

Sequence Listing

<110> Baker, Kevin P.
 Botstein, David
 Desnoyers, Luc
 Eaton, Dan L.
 Ferrara, Napoleone
 Fong, Sherman
 Gao, Wei-Qiang
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, Christopher J.
 Gurney, Austin L.
 Hillan, Kenneth J.
 Pan, James
 Paoni, Nicholas F.
 Roy, Margaret Ann
 Smith, Victoria
 Stewart, Timothy A.
 Tumas, Daniel
 Watanabe, Colin K.
 Williams, P. Mickey
 Wood, William I.

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35 40 45
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50 55 60
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80 85 90
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<210> 12
 <211> 699
 <212> PRT
 <213> Homo sapiens

<220>
 <221> TRANSMEM
 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

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 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys
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				125					130					135
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro
				140					145					150
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro
				155					160					165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly
				170					175					180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro
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Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly
				200					205					210
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg
				215					220					225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln
				230					235					240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp
				245					250					255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly
				260					265					270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe
				275					280					285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile
				290					295					300
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser
				305					310					315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu
				320					325					330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu
				335					340					345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn
				350					355					360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser
				365					370					375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr
				380					385					390
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His Pro Leu Pro Ile Trp Thr Pro Ala
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<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
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<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgaagt gtttggcctc ggte 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
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ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgtg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

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aaaaaaaaaa aaaaaaaaaa aaaa 1524

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<210> 17
<211> 327
<212> PRT
<213> Homo sapiens
<220>

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<222> 1-24
 <223> Synthetic construct

<400> 19
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<210> 20
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

<400> 20
 cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
 <211> 494
 <212> DNA
 <213> Homo sapiens

<400> 21
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 gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
 gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200
 tgccatgacc tgcagccaag cccagccccg tggggaaggg gagaaagtgg 250
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 ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
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<210> 22
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-15
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

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Ser	Cys	Leu	Glu	Trp	Gly	Leu	Val	Gly	Ala	Gln	Lys	Val	Ser
			20					25					30
Ala	Thr	Asp	Ala	Pro	Ile	Arg	Asp	Trp	Ala	Phe	Phe	Pro	Ser
			35					40					45
Phe	Leu	Cys	Leu	Leu	Pro	His	Arg	Pro	Ala	Met	Thr	Cys	Gln
			50					55					60
Ala	Gln	Pro	Arg	Gly	Glu	Gly	Glu	Lys	Val	Gly	Asp	Gly	
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<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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<210> 24
 <211> 616
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-33
 <223> Signal peptide.

<220>
 <221> TRANSMEM
 <222> 13-40
 <223> Transmembrane domain (type II).

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 20 25 30
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
 35 40 45
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
 50 55 60
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
 65 70 75
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
 80 85 90

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Gln	Asp	Glu	Arg	Lys	Ala	Trp	Arg	Arg	Cys	Asp	Arg	Gly	Gly	Phe					
				395					400					405					
Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val					
				410					415					420					
Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr					
				425					430					435					
Asn	Ala	Val	Ala	Thr	Ala	Arg	Gln	Leu	Leu	Ala	Tyr	Thr	Val	Glu					
				440					445					450					
Ala	Ala	Asn	Phe	Ser	Asp	Lys	Met	Asp	Val	Ile	Phe	Val	Ala	Glu					
				455					460					465					
Met	Ile	Glu	Lys	Phe	Gly	Arg	Phe	Thr	Lys	Glu	Glu	Lys	Ser	Lys					
				470					475					480					
Glu	Leu	Gly	Asp	Val	Met	Val	Asp	Ile	Ala	Ser	Asn	Ile	Met	Leu					
				485					490					495					
Ala	Asp	Glu	Arg	Val	Leu	Trp	Leu	Ala	Gln	Arg	Glu	Ala	Lys	Ala					
				500					505					510					
Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg					
				515					520					525					
Leu	Ala	Gly	Gly	Ala	His	Val	Tyr	Ser	Thr	Tyr	Ser	Pro	Asn	Ile					
				530					535					540					
Ala	Leu	Glu	Ala	Tyr	Val	Ile	Lys	Ser	Thr	Gly	Phe	Thr	Gly	Met					
				545					550					555					
Thr	Cys	Thr	Val	Phe	Gln	Lys	Val	Ala	Ala	Ser	Asp	Arg	Thr	Gly					
				560					565					570					
Leu	Ser	Asp	Tyr	Gly	Arg	Arg	Asp	Pro	Glu	Gly	Asn	Leu	Asp	Lys					
				575					580					585					
Gln	Leu	Ser	Phe	Lys	Cys	Asn	Val	Ser	Asn	Thr	Phe	Ser	Ser	Leu					
				590					595					600					
Ala	Leu	Lys	Val	Cys	Tyr	Ile	Leu	Gln	Ser	Phe	Lys	Thr	Ile	Tyr					
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Ser

<210> 25
 <211> 24
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-24

<210> 29
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-21
<223> Signal peptide.

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Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
35 40 45
Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
50 55 60
Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
65 70 75
Lys Gly Ser Gln Lys Ser
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<210> 30
<211> 2128
<212> DNA
<213> Homo sapiens

<400> 30
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Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu
				230					235					240
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu
				245					250					255
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln
				260					265					270
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr
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Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr
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Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala
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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
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Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
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Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
				125					130					135
Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
				140					145					150
Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165
Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
				170					175					180
Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
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His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
				200					205					210
Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
				215					220					225
Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
				230					235					240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
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Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
320 325 330

Glu Pro Glu Glu Gln
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<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
tgctctttgt cccagacttc tgtcc 25

<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
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<210> 36
<211> 25
<212> DNA
<213> Artificial

<220>
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<222> 1-25
<223> Synthetic construct.

<400> 36

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 <213> Artificial
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 <222> 1-23
 <223> Synthetic construct.
 <400> 37
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 <210> 38
 <211> 39
 <212> DNA
 <213> Artificial
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 <222> 1-39
 <223> Synthetic construct.
 <400> 38
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 <223> Synthetic construct.
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 <211> 2084
 <212> DNA
 <213> Homo sapiens
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<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
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35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu
200 205 210

Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn
215 220 225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe
230 235 240

Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu
245 250 255

Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser
260 265 270

His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu
275 280 285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser
290 295 300

Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu
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Arg Thr Ser Val

<210> 42
<211> 1594
<212> DNA
<213> Homo sapiens

<400> 42
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<210> 43
<211> 263
<212> PRT
<213> Homo sapiens

<400> 43
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Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50										55					60				
Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr					
				65					70					75					
Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys					
				80					85					90					
Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu					
				95					100					105					
Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp					
				110					115					120					
Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp					
				125					130					135					
Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr					
				140					145					150					
Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu					
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Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe					
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Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val					
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Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn					
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Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe					
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Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile					
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				260															

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<212> DNA

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<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

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<212> DNA
<213> Artificial

<220>
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<222> 1-20
<223> Synthetic construct.

<400> 45
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<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
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<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
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<223> Synthetic construct.

<400> 47
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<210> 48
<211> 25
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<213> Artificial

<220>
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<222> 1-25
<223> Synthetic construct.

<400> 48
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<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

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aaaaaaaaaa aaaaaaaga 1969

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<211> 283
<212> PRT
<213> Homo sapiens

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35 40 45
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
50 55 60
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
65 70 75
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
80 85 90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
95 100 105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
110 115 120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
125 130 135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
140 145 150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
155 160 165

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr
170 175 180
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp
185 190 195
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys
200 205 210
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro
215 220 225
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
230 235 240
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly
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<211> 1734
<212> DNA
<213> Homo sapiens

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<210> 52

<211> 440

<212> PRT

<213> Homo sapiens

<400> 52

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				20					25					30
Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp
				35					40					45
Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly

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Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly	80	90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala	95	105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val	110	120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val	125	135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile	140	150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro	155	165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser	170	180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln	185	195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly	200	210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln	215	225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly	230	240
Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser	245	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly	260	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser	275	285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser	290	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly	305	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His	320	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly	335	345

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<212> PRT
<213> Homo sapiens

<210> 55
 <211> 2401
 <212> DNA
 <213> Homo sapiens

<400> 55
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<212> PRT
<213> Homo sapiens

<400> 56
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35 40 45

Pro Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr Val Pro
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Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys Val
65 70 75

Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro
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Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro
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Thr Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg
110 115 120

Val Val Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln
125 130 135

Glu Phe Val Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly
140 145 150

Pro Pro Ser Lys Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val
155 160 165

Ile Gln Arg Ala Gly Leu Val Phe Pro Asn Met Glu Ala Tyr Ala
170 175 180

Val Ser Pro Gly Arg Met Arg Gln Phe Asp Asp Leu Phe Arg Gly
185 190 195

Glu Thr Gly Lys Asp Arg Glu Lys Ser His Ser Trp Leu Ser Thr
200 205 210

Gly Trp Phe Thr Met Val Ile Ala Val Glu Leu Cys Asp His Val
215 220 225

His Val Tyr Gly Met Val Pro Pro Asn Tyr Cys Ser Gln Arg Pro
230 235 240

Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr Glu Pro Lys Gly Pro
245 250 255

Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His Ser Arg Lys Gly
260 265 270

Asn His His Arg Phe Ile Thr Glu Lys Arg Val Phe Ser Ser Trp
275 280 285

Ala Gln Leu Tyr Gly Ile Thr Phe Ser His Pro Ser Trp Thr
290 295

<210> 57
<211> 4277
<212> DNA
<213> Homo sapiens

<400> 57

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gaagtcttgt cgacatttat accgtctgag ggtagcagct cgaaactaga 250
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<210> 58
 <211> 1115

<212> PRT
<213> Homo sapiens

<400> 58

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Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	35	40	45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	50	55	60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	65	70	75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	80	85	90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	95	100	105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	110	115	120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	125	130	135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	140	145	150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	155	160	165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	170	175	180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	185	190	195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	200	205	210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	215	220	225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	230	235	240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	245	250	255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	260	265	270	

560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile Gln	
575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro Asp	
590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr Ile	
605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro Arg	
620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr Lys	
635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala Ile	
650	655	660
Pro Pro Ser Arg Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys Gly	
665	670	675
Thr Ser Tyr Lys Phe Arg Val Arg Ala	Leu Asn Met Leu Gly Glu	
680	685	690
Ser Glu Pro Ser Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly Tyr	
695	700	705
Ser Gly Arg Val Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile Thr	
710	715	720
Phe Thr Asp Ala Val Asn Glu Thr Thr	Ile Met Leu Lys Trp Met	
725	730	735
Tyr Ile Pro Ala Ser Asn Asn Asn Thr	Pro Ile His Gly Phe Tyr	
740	745	750
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr Lys	
755	760	765
Lys Asp Met Val Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser His	
770	775	780
Leu Gln Pro Glu Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe Asn	
785	790	795
Glu Gly Gly Glu Ser Glu Phe Ser Asn	Val Met Ile Cys Glu Thr	
800	805	810
Lys Ala Arg Lys Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro Pro	
815	820	825
Thr Leu Ala Pro Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu Arg	
830	835	840
Pro Val Gly Thr Gly Ala Met Val Ala	Arg Ser Ser Asp Leu Pro	
845	850	855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile
 860 865 870
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 875 880 885
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro
 890 895 900
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His
 905 910 915
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala
 920 925 930
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala
 935 940 945
 Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
 950 955 960
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
 965 970 975
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
 980 985 990
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
 995 1000 1005
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
 1010 1015 1020
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
 1025 1030 1035
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
 1040 1045 1050
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
 1055 1060 1065
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
 1070 1075 1080
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
 1085 1090 1095
 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
 1100 1105 1110
 Pro Pro Leu Thr Ile
 1115

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 59
 gggaacacaca gcagtcattg cctgc 25

 <210> 60
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 60
 gcacacgtag cctgtcgctg gaggc 24

 <210> 61
 <211> 42
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-42
 <223> Synthetic construct.

 <400> 61
 caccacaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

 <210> 62
 <211> 1661
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 678
 <223> unknown base

 <400> 62
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 caccggccgc gaggggtccc gcgcgctcag ccggcggtat ctgcggcgctc 150
 tgctgtcctt gctactgctg ctgctgctgc ggcagcccggt aaccgcgcgcg 200
 gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccccag 250
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 ctacgccagg caccacaaa accctggacc ttcggggctcg cgcgcaggcc 350

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cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
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gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
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gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
cacatggaaa a 1661

<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

<220>

<221> unsure

<222> 196, 386

<223> unknown amino acid

<400> 63

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Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	20	25	30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	35	40	45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	50	55	60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	65	70	75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	80	85	90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	95	100	105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	110	115	120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	125	130	135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	140	145	150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	155	160	165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	170	175	180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	185	190	195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	200	205	210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	215	220	225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	230	235	240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	245	250	255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala				

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu	Glu Val Ser Gln Ala Pro	
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg	Ala Val Cys Asp Asn Leu	
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln	Leu Leu Lys Asn Gly Gly	
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly	Val Leu Gln Cys Asn Leu	
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp	His Phe Asp His Ile Arg	
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp	
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr	
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu Glu	
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg	
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro Val	
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His Ser	
425	430	435
His Leu Val Pro Gln Asn Gly His Gln	Ala Thr His Leu Glu Val	
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn Ala	
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val	Ala Ala Ala Thr Ile Pro	
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 65
 gtcacacaca gctctggcag ctgag 25

<210> 66
 <211> 47
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 66
 ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67
 <211> 1564
 <212> DNA
 <213> Homo sapiens

<400> 67
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 aacaccacaca gatccctcta tgactgcaat gtgagggtgc cggctttgct 100
 ggcccagcaa gcctgataag catgaagctc ttatcttttg tggctgtggt 150
 cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
 tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
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atcggcacia gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700
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<210> 68
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
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 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
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 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
65 70 75
Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
80 85 90
Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
95 100 105
Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
110 115 120
Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
125 130 135
Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
140 145 150
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
155 160 165
Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
170 175 180
Met Leu Ser

<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

<400> 69
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<210> 70
<211> 259
<212> PRT
<213> Homo sapiens

<400> 70
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20 25 30
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
50 55 60

Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
65 70 75

Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
80 85 90

His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
95 100 105

Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
110 115 120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
125 130 135

Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
140 145 150

Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
155 160 165

Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
170 175 180

Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
185 190 195

Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
200 205 210

Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
215 220 225

Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
230 235 240

Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
245 250 255

Cys Gln Lys Ile

<210> 71
<211> 1809
<212> DNA
<213> Homo sapiens

<400> 71
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ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys
230 235 240

Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala
245 250 255

Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser
260 265 270

Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser
275 280 285

Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln
290 295 300

Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn
305 310 315

Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr
320 325 330

Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg
335 340 345

Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp
350 355 360

Leu Ile Arg

<210> 73
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 73
aatcatggc aaatatttcc cttccc 26

<210> 74
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 74
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<210> 75
<211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
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<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu
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Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
20 25 30

Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45

Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60

Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His	80	85	90
Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His	95	100	105
Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg	110	115	120
Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro	125	130	135
Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78

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gccattgggt caaggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79
<211> 475
<212> PRT
<213> Homo sapiens

<400> 79
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Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
35 40 45
Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
50 55 60
Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
65 70 75
Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
80 85 90
Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
95 100 105

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

[illegible]

				395					400					405
Thr	Val	Val	Phe	Gln 410	Ser	Asp	Val	Tyr	Pro 415	Ala	Leu	Leu	Ser	Ser 420
Leu	Leu	Gly	Leu	Ser 425	Asn	Gly	Tyr	Leu	Ser 430	Thr	Leu	Ala	Leu	Leu 435
Tyr	Gly	Pro	Lys	Ile 440	Val	Pro	Arg	Glu	Leu 445	Ala	Glu	Ala	Thr	Gly 450
Val	Val	Met	Ser	Phe 455	Tyr	Val	Cys	Leu	Gly 460	Leu	Thr	Leu	Gly	Ser 465
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<210> 80
<211> 22
<212> DNA
<213> Artificial
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<223> Synthetic construct.
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```
<210> 81
<211> 23
<212> DNA
<213> Homo sapiens
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<222> 1-23  
<223> Synthetic construct.
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cgtaggtgac acagaagccc agg 23
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<210>	82
<211>	49
<212>	DNA
<213>	Artificial

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<222> 1-49
<223> Synthetic construct.
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<210> 83
<211> 1844

<212> DNA
<213> Homo sapiens

<400> 83

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<210> 84
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 84
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 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
 35 40 45
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu	170	175	180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys	185	190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu	Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala	Met Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala	Ala Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu			

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly	Arg Ile Tyr Phe Ala Gly	
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp	Val Glu Thr Ala Val Lys	
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile	Asn Ser Arg Lys Gly Pro	
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly	His Ala Ser Asp Met Glu	
515	520	525
Gly Gln Gly His Val His Gly Val Ala	Ser Ser Pro Ser His Asp	
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Leu Ala Lys Glu Glu Gly Ser His Pro	Pro Val Gln Gly Gln Leu	
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Ser Leu Gln Asn Thr Thr His Thr Arg	Thr Ser His	
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<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

Met	Asp	Ala	Leu	Lys	Pro	Pro	Cys	Leu	Trp	Arg	Asn	His	Glu	Arg
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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
				20					25					30

[illegible]

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His	Gln	Asn	Ile	Val 335	Ser	Asn	Ala	Ala	Ala 340	Phe	Leu	Lys	Cys	Val 345
Glu	His	Ala	Tyr	Glu 350	Pro	Thr	Pro	Asp	Asp 355	Val	Ala	Ile	Ser	Tyr 360
Leu	Pro	Leu	Ala	His 365	Met	Phe	Glu	Arg	Ile 370	Val	Gln	Ala	Val	Val 375
Tyr	Ser	Cys	Gly	Ala 380	Arg	Val	Gly	Phe	Phe 385	Gln	Gly	Asp	Ile	Arg 390
Leu	Leu	Ala	Asp	Asp 395	Met	Lys	Thr	Leu	Lys 400	Pro	Thr	Leu	Phe	Pro 405
Ala	Val	Pro	Arg	Leu 410	Leu	Asn	Arg	Ile	Tyr 415	Asp	Lys	Val	Gln	Asn 420
Glu	Ala	Lys	Thr	Pro 425	Leu	Lys	Lys	Phe	Leu 430	Leu	Lys	Leu	Ala	Val 435
Ser	Ser	Lys	Phe	Lys 440	Glu	Leu	Gln	Lys	Gly 445	Ile	Ile	Arg	His	Asp 450
Ser	Phe	Trp	Asp	Lys 455	Leu	Ile	Phe	Ala	Lys 460	Ile	Gln	Asp	Ser	Leu 465
Gly	Gly	Arg	Val	Arg 470	Val	Ile	Val	Thr	Gly 475	Ala	Ala	Pro	Met	Ser 480
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Thr	Leu	Pro	Gly	Asp 515	Trp	Thr	Ser	Gly	His 520	Val	Gly	Val	Pro	Leu 525
Ala	Cys	Asn	Tyr	Val 530	Lys	Leu	Glu	Asp	Val 535	Ala	Asp	Met	Asn	Tyr 540
Phe	Thr	Val	Asn	Asn 545	Glu	Gly	Glu	Val	Cys 550	Ile	Lys	Gly	Thr	Asn 555
Val	Phe	Lys	Gly	Tyr 560	Leu	Lys	Asp	Pro	Glu 565	Lys	Thr	Gln	Glu	Ala 570
Leu	Asp	Ser	Asp	Gly 575	Trp	Leu	His	Thr	Gly 580	Asp	Ile	Gly	Arg	Trp 585
Leu	Pro	Asn	Gly	Thr 590	Leu	Lys	Ile	Ile	Asp 595	Arg	Lys	Lys	Asn	Ile 600
Phe	Lys	Leu	Ala	Gln 605	Gly	Glu	Tyr	Ile	Ala 610	Pro	Glu	Lys	Ile	Glu 615

Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His
620 625 630

Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp
635 640 645

Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly
650 655 660

Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile
665 670 675

Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr
680 685 690

Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser
695 700 705

Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly
710 715 720

Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu
725 730 735

His Ile Gln Asp

<210> 87
<211> 2725
<212> DNA
<213> Homo sapiens

<400> 87
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 <212> PRT
 <213> Homo sapiens

<400> 88
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 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
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Thr	Tyr	Ser	Pro	His 155	Glu	Asp	Glu	Ala	Met 160	Val	Leu	Phe	Leu	Asn 165
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Leu	Gly	Ser	Gln	Ala 200	Gly	Pro	Ala	Leu	Gly 205	Trp	Arg	Asp	Thr	Trp 210
Ala	Phe	Val	Gly	Arg 215	Lys	Gly	Gly	Pro	Val 220	Phe	Gly	Glu	Lys	His 225
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Val	Leu	Glu	Glu	Asp 395	Leu	Asp	Ile	Ala	Val 400	Asp	Phe	Phe	Ser	Phe 405
Leu	Ser	Gln	Ser	Ile 410	His	Leu	Leu	Glu	Glu 415	Asp	Asp	Ser	Leu	Tyr 420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu

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Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly		
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Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala		
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Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu		
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Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr		
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Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp		
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp		
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Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe		
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Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro		
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 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.
 <400> 89

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<210>	90
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<212>	DNA
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<212> DNA
<213> Artificial
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<223> Synthetic construct.
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<213> Artificial
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<223> Synthetic construct.
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<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens
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<400> 94

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Asn	Ala Thr Gly Val	Ala Met Leu Phe	Ser	Ala Gly Thr Phe	Leu
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Tyr	Val Ala Thr Val	His Val Leu Pro	Glu	Val Gly Gly Ile	Gly
	260		265		270
His	Ser His Lys Pro	Asp Ala Thr Gly	Gly	Arg Gly Leu Ser	Arg
	275		280		285
Leu	Glu Val Ala Ala	Leu Val Leu Gly	Cys	Leu Ile Pro Leu	Ile
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<223> Synthetic construct.

<400> 96
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<212> DNA
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<220>
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<223> Synthetic construct.

<400> 97
ctgtgctcat gttcatggac aactg 25

<210> 98
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<212> DNA
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<220>
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<223> Synthetic construct.

<400> 98
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<210> 99
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<212> DNA
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<211> 401
<212> PRT
<213> Homo sapiens

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Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
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Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
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<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
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Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
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Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
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Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
				95					100					105
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
				110					115					120
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
				125					130					135
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
				140					145					150
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
				155					160					165
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp
				170					175					180
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe
				185					190					195
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly

				200					205					210
Ile	Leu	Glu	His	Leu 215	Tyr	Pro	Thr	Met	Asp 220	Ser	Gly	Glu	Trp	Asp 225
Val	Leu	Ile	Ala	His 230	Phe	Leu	Gly	Val	Asp 235	His	Cys	Gly	His	Lys 240
His	Gly	Pro	His	His 245	Pro	Glu	Met	Ala	Lys 250	Lys	Leu	Ser	Gln	Met 255
Asp	Gln	Val	Ile	Gln 260	Gly	Leu	Val	Glu	Arg 265	Leu	Glu	Asn	Asp	Thr 270
Leu	Leu	Val	Val	Ala 275	Gly	Asp	His	Gly	Met 280	Thr	Thr	Asn	Gly	Asp 285
His	Gly	Gly	Asp	Ser 290	Glu	Leu	Glu	Val	Ser 295	Ala	Ala	Leu	Phe	Leu 300
Tyr	Ser	Pro	Thr	Ala 305	Val	Phe	Pro	Ser	Thr 310	Pro	Pro	Glu	Glu	Pro 315
Glu	Val	Ile	Pro	Gln 320	Val	Ser	Leu	Val	Pro 325	Thr	Leu	Ala	Leu	Leu 330
Leu	Gly	Leu	Pro	Ile 335	Pro	Phe	Gly	Asn	Ile 340	Gly	Glu	Val	Met	Ala 345
Glu	Leu	Phe	Ser	Gly 350	Gly	Glu	Asp	Ser	Gln 355	Pro	His	Ser	Ser	Ala 360
Leu	Ala	Gln	Ala	Ser 365	Ala	Leu	His	Leu	Asn 370	Ala	Gln	Gln	Val	Ser 375
Arg	Phe	Leu	His	Thr 380	Tyr	Ser	Ala	Ala	Thr 385	Gln	Asp	Leu	Gln	Ala 390
Lys	Glu	Leu	His	Gln 395	Leu	Gln	Asn	Leu	Phe 400	Ser	Lys	Ala	Ser	Ala 405
Asp	Tyr	Gln	Trp	Leu 410	Leu	Gln	Ser	Pro	Lys 415	Gly	Ala	Glu	Ala	Thr 420
Leu	Pro	Thr	Val	Ile 425	Ala	Glu	Leu	Gln	Gln 430	Phe	Leu	Arg	Gly	Ala 435
Arg	Ala	Met	Cys	Ile 440	Glu	Ser	Trp	Ala	Arg 445	Phe	Ser	Leu	Val	Arg 450
Met	Ala	Gly	Gly	Thr 455	Ala	Leu	Leu	Ala	Ala 460	Ser	Cys	Phe	Ile	Cys 465
Leu	Leu	Ala	Ser	Gln 470	Trp	Ala	Ile	Ser	Pro 475	Gly	Phe	Pro	Phe	Cys 480
Pro	Leu	Leu	Leu	Thr 485	Pro	Val	Ala	Trp	Gly 490	Leu	Val	Gly	Ala	Ile 495

Ala Tyr Ala Gly	Leu Leu Gly Thr Ile	Glu Leu Lys Leu Asp	Leu
500		505	510
Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe
515		520	525
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala
530		535	540
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu Leu	Phe
545		550	555
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala
560		565	570
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val
575		580	585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu
590		595	600
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg
605		610	615
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu
620		625	630
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr
635		640	645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met
650		655	660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala
665		670	675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg
680		685	690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg
695		700	705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala
710		715	720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu
725		730	735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
740		745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
755		760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
770		775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr

785					790					795				
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met	Gln	Glu	Glu	Phe	Arg	Gly
				800					805					810
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly	Pro	Leu	Thr	Val	Ala	Ala
				815					820					825
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala	Ala	Met	Val	Thr	Ala	Leu
				830					835					840
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile
				845					850					855
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu	Gln	Ser	Phe	Leu	Leu	Leu
				860					865					870
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val	Thr	Thr	Pro	Gly	Pro	Phe
				875					880					885
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr
				890					895					900
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile
				905					910					915
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser
				920					925					930
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val	Gly	Ala	Asn	Thr	Phe	Ala
				935					940					945
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys	Pro	Leu	Leu	Leu	Leu	Trp
				950					955					960
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Gln	Gln	Pro
				965					970					975
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu
				980					985					990
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg	Asp	Ala	Pro	Gln	His	Phe
				995					1000					1005
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu
				1010					1015					1020
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg
				1025					1030					1035
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe
				1040					1045					1050
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly
				1055					1060					1065
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe
				1070					1075					1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
tgccgctgcc gccgctgctg ctgttgctcc tggcggcgcc ttggggacgg 50
gcagttccct gtgtctctgg tggtttgcc aaacctgcaa acatcacctt 100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtcatt tctgttgctc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatcaaac agaacgtggt ccagtggtg gaccaaccac acgctggtgc 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc ccctcgccg tgcctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcaccctca atatctcgga tgattctaaa 750
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcgggaacct gaggccccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctt 950
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcgtt 1100
ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccg 1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

agccttctga gggggatggg ctcgagagg agggctcttct atctagactc 1350
 tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400
 catgcaattc atggaggaat ggggggttata tgtgcagatg gaaaactgat 1450
 gccaacactt ccttttgcct tttgtttcct gtgcaaacia gtgagtcacc 1500
 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550
 ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600
 cgtgtgtgat tggttcatgc atgtaggctc cttacaatg atggtgggcc 1650
 tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700
 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104
 <211> 442
 <212> PRT
 <213> Homo sapiens

<400> 104
 Met Ser Tyr Asn Gly Leu His Gln Arg Val Phe Lys Glu Leu Lys
 1 5 10 15
 Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu
 20 25 30
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
 95 100 105
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
 110 115 120
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
 125 130 135
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
 140 145 150
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
 155 160 165

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile	170	175	180
Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys	185	190	195
Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys	200	205	210
Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val	215	220	225
Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro	230	235	240
Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu	245	250	255
Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser	260	265	270
Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys	275	280	285
Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys	290	295	300
Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser	305	310	315
Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu	320	325	330
Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp	335	340	345
Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro	350	355	360
Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr	365	370	375
Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser	380	385	390
Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly	395	400	405
Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro	410	415	420
Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly	425	430	435
Leu Tyr Val Gln Met Glu Asn	440		

<210> 105

<211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-21
 <223> Synthetic construct

<400> 105
 cgctgctgct gttgctcctg g 21

<210> 106
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 106
 cagtgtgccca ggactttg 18

<210> 107
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 107
 agtcgcaggc agcgttg 18

<210> 108
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 108
 ctcctccgag tctgtgtgct cctgc 25

<210> 109
 <211> 51
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-51

<223> Synthetic construct.

<400> 109

ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacat 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

cggacgcgtg ggccggacgcg tgggcccgcg cgtgggtctc tgcggggaga 50
 cggcagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
 tctgctgact gtggccaccg cctgatgct gcccgtaag cccccgcag 150
 gctcctgggg ggcccagatc atcgggggccc acgaggtgac cccccactcc 200
 aggccttaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250
 ctctctgctg cgagcccgtt ggggtggtctc ggccgcccac tgcttcagcc 300
 acagagacct ccgactggc ctggtggtgc tgggcgcccac cgtcctgagt 350
 actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400
 ccccgactac caccatga cccacgcca cgacatctgc ctgctgcggc 450
 tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggtgcca 500
 gggagaaggg ccaggcccc caccgcccgg acacggtgcc ggggtggctgg 550
 ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600
 ccaaggtccg agtctgagc ccggacgtct gcaacagctc ctggaagggc 650
 cacctgacac ttaccatgct ctgcacccgc agtggggaca gccacagacg 700
 gggcttctgc tcggccgact ccggaggggcc cctggtgtgc aggaaccggg 750
 ctacaggcct cgtttccttc tcgggcctct ggtgcggcga cccaagacc 800
 cccgacgtgt acacgcagg gtccgccttt gtggcctgga tctgggacgt 850
 ggttcggcgg agcagtcctc agcccggccc cctgcctggg accaccaggc 900
 cccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950
 gccgtccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000
 tgttcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050
 tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val	1	5	10	15
Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp	20	25	30	
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg	35	40	45	
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly	50	55	60	
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys	65	70	75	
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala	80	85	90	
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile	95	100	105	
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala	110	115	120	
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly	125	130	135	
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro	140	145	150	
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val	155	160	165	
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val	170	175	180	
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His	185	190	195	
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg	200	205	210	
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg	215	220	225	
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly	230	235	240	
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val	245	250	255	

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
 275 280

<210> 112
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 112
 gacgtctgca acagtcctg gaag 24

<210> 113
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 113
 cgagaaggaa acgaggccgt gag 23

<210> 114
 <211> 44
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-44
 <223> Synthetic construct.

<400> 114
 tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

<400> 115
 gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50
 cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100
 cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
 tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acgggcgcca acacagggcat cgggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
 tgtcaacgcc cggcacctgg acttggttcc cctcaagtct atccgagagt 400
 ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450
 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500
 gatgcagttt ggcgttaacc acctgggtca ctttctcttg aaaaacttgc 550
 tgctggacaa gctgaaagcc tcagcccctt cgcggatcat caacctctcg 600
 tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650
 gacgaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700
 tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750
 actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800
 cacgggcac catggttcca ctttctccag caccacactc gggcccatct 850
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 ctggccgtgg cggaggaact ggcggatgtt tccggaaagt acttcgatgg 950
 actcaaacag aaggccccgg ccccgaggc tgaggatgag gaggtggccc 1000
 ggaggctttg ggctgaaagt gcccgctgg tgggcttaga ggctccctct 1050
 gtgaggagc agcccctccc cagataacct ctggagcaga tttgaaagcc 1100
 aggatggcgc ctccagaccg aggacagctg tccgccatgc ccgcagcttc 1150
 ctggcactac ctgagccggg agaccagga ctggcggccg ccatgcccgc 1200
 agtaggttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250
 gcaactgccc gggctctggc tggttccgtc tgctctgctg ccagcagggg 1300
 agaggggcca tctgatgctt cccctgggaa tctaaactgg gaatggccga 1350
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 gcctgtcggg gaggttcca agtggtccg tgaagagcat gggcaagttg 1450
 tctgacactt ggtggattct tgggtccctg tgggaccttg tgcattcatg 1500
 gtctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550
 ctgtctccca tgatggtgtg gtacagcgag ctgttgctg gctatggcat 1600
 ggctgtgccg ggggtgtttg ctgagggtt cctgtgccag agcccagcca 1650

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
 1 5 10 15
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
 20 25 30
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225


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agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750
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aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
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cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050
tagcctgact cccagaactt taagactttc tccccactgc cttctgctgc 2100
agccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

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<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala	1	5	10	15
Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr	20	25	30	
Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg	35	40	45	
Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala	50	55	60	
Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu	65	70	75	
His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe	80	85	90	
Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His	95	100	105	
Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr	110	115	120	
Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly	125	130	135	
Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn	140	145	150	
Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser	155	160	165	
Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr	170	175	180	
Gly	Asp	Asp	Cys	Phe	Gln	Val	Gly	Lys	Val	Ala	Tyr	Asp	Met	Gly	185	190	195	
Asp	Tyr	Tyr	His	Ala	Ile	Pro	Trp	Leu	Glu	Glu	Ala	Val	Ser	Leu	200	205	210	
Phe	Arg	Gly	Ser	Tyr	Gly	Glu	Trp	Lys	Thr	Glu	Asp	Glu	Ala	Ser	215	220	225	
Leu	Glu	Asp	Ala	Leu	Asp	His	Leu	Ala	Phe	Ala	Tyr	Phe	Arg	Ala	230	235	240	

Gly Asn Val Ser	Cys Ala Leu Ser Leu	Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp	Asn Lys Arg Met Ala	Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu	Ala Glu Ser Pro Asn	His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg	Pro Asn Ile Pro His	Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu	Cys Gln Thr Leu Gly	Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser	Leu Tyr Cys Ser Tyr	Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu	Gln Pro Ile Arg Lys	Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala	Leu Tyr His Asp Phe	Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg	Glu Leu Ala Glu Pro	Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly	Glu Lys Gln Leu Gln	Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp	Leu Lys Asp Thr Val	Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg	Ile Ala Ala Leu Thr	Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu	Tyr Leu Gln Val Val	Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro	His Phe Asp His Ala	Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met	Lys Ser Gly Asn Arg	Val Ala Thr Phe Met Ile	455	460	465
Tyr Leu Ser Ser	Val Glu Ala Gly Gly	Ala Thr Ala Phe Ile Tyr	470	475	480
Ala Asn Leu Ser	Val Pro Val Val Arg	Asn Ala Ala Leu Phe Trp	485	490	495
Trp Asn Leu His	Arg Ser Gly Glu Gly	Asp Ser Asp Thr Leu His	500	505	510
Ala Gly Cys Pro	Val Leu Val Gly Asp	Lys Trp Val Ala Asn Lys	515	520	525
Trp Ile His Glu	Tyr Gly Gln Glu Phe	Arg Arg Pro Cys Ser Ser			

530

535

540

Ser Pro Glu Asp

<210> 119
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 119
cgggacagga gacccagaaa ggg 23

<210> 120
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 120
ggccaagtga tccaaggcat cttc 24

<210> 121
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-49
<223> Synthetic construct.

<400> 121
ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattgggg 49

<210> 122
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 122
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tccccccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100
gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
ggagagcccc ggagcccccg taacccgogc ggggagcgcc caggatgccg 200

cgcgggggact	cggagcaggt	gcgctactgc	gcgcgcttct	cctacctctg	250
gctcaagttt	tcacttatca	tctattccac	cgtgttctgg	ctgattgggg	300
ccctggtcct	gtctgtgggc	atctatgcag	aggttgagcg	gcagaaatat	350
aaaacccttg	aaagtgcctt	cctggctcca	gccatcatcc	tcatcctcct	400
gggcgtcgtc	atgttcatgg	tctccttcat	tgggtgtgctg	gcgtccctcc	450
gtgacaacct	gtaccttctc	caagcattca	tgtacatcct	tgggatctgc	500
ctcatcatgg	agctcattgg	tggcgtgggtg	gccttgacct	tccggaacca	550
gaccattgac	ttcctgaacg	acaacattcg	aagaggaatt	gagaactact	600
atgatgatct	ggacttcaaa	aacatcatgg	actttgttca	gaaaaagttc	650
aagtgtctgtg	gcgggggagga	ctaccgagat	tggagcaaga	atcagtacca	700
cgactgcagt	gcccctggac	ccctggcctg	tggggtgccc	tacacctgct	750
gcatacaggaa	cacgacagaa	gttgtcaaca	ccatgtgtgg	ctacaaaact	800
atcgacaagg	agcgtttcag	tgtgcaggat	gtcatctacg	tgcggggctg	850
caccaacgcc	gtgatcatct	ggttcatgga	caactacacc	atcatggcgt	900
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ctgctgtaca	tcaccgggt	ggaggacatc	atcatggagc	actctgtcac	1000
tgatgggctc	ctggggcccg	gtgccaagcc	cagcgtggag	gcggcaggca	1050
cgggatgctg	cttgtgtctac	cccaattagg	gccagcctg	ccatggcagc	1100
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ggggagaggg	agtgtgcccc	tcggggcagg	agggaaagggc	atctggggaa	1500
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tccttgagcc	tagttttttt	ttacgtgatt	tttgtaacat	tcattttttt	1650

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 catgttttgt tttgttttta aaaaaaaa 1778

<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123
 Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe
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 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcattctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50
gctgccctct gacacctggg aagatggccg gcccgaggac cttcacccctt 100
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtcccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggct atcacagcta 350
acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctgggtcaa 450
gaccatcgtg gaggttccaca tgacgactga ggccaagcc accatccgca 500
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<210> 128
<211> 484
<212> PRT
<213> Homo sapiens

<400> 128
Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala
1 5 10 15
Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
20 25 30
Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
35 40 45
Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
50 55 60
Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
65 70 75
Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
80 85 90
Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
95 100 105
Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
110 115 120
Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
125 130 135
Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
140 145 150
Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
155 160 165
Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
170 175 180
Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
185 190 195
Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
200 205 210
Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
215 220 225

135

<400> 129
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gtggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccccaaag 100
aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150
ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200
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agatcctggc aaactcctgg cgataactcca gtgcattcac caacaggata 350
ttttttgcca tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400
aaacatgaat tcagctccaa ctttcatcaa ctttcttgca aaagggaaac 450
ccaaacgggg tgatacatat gagttacagg tgcgggggtt ttcagctgag 500
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550
tagacccccca aattatgctg gtcccccttat gttgggattg cttttggctg 600
ttattggtgg acttgtgtat cttcgaagaa gtaatatgga atttctcttt 650
aataaaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700
atctggtcaa atgtggaacc atataagagg accaccatat gcccataaga 750
atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800
tttgtagctg aaacacacat tgttcttctg tttaatggtg gagttacctt 850
aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900
agcgaaagat aatgtgtgtg gctggtattg gacttgttgt attattcttc 950
agttggatgc tctctatttt tagatctaaa tatcatggct acccatacag 1000
ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050
ggaaattgaa aaacgaaaat cgtgtgtgtt tgaaaagaag aatgcaactt 1100
gtatattttg tattacctct ttttttcaag tgatttaa atgttaatcat 1150
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aactactact ttgttttagt tagaacaag ctcaaaacta ctttagttaa 1350
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cctgaccagg tgttcccaca tatgcctgtt acagataact acattaggaa 1450

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ctcctcctcc ttgcatattt cctactgcgc tccagcctga gtgatagagt 1650
gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700
gcttgagtat ggtgttaact accttgtatt tagaaagatt tcagattcat 1750
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aaattagagt ttgtcactta ttccatttgt acctaagaga aaaataggct 1900
cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950
tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000
gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050
attagctggg tgtggtggca ggagcctgta atcccagcta cacaggaggc 2100
tgaggcacga gaatcacttg aactcaggag atggagggtt cagtgagccg 2150
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aaaaaaaaa aaa 2213

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<210> 130
<211> 335
<212> PRT
<213> Homo sapiens

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<400> 130
Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
  1             5             10             15
Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
             20             25             30
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
             35             40             45
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
             50             55             60
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
             65             70             75
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
             80             85             90
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
             95            100            105

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Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp
				110					115					120
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser
				125					130					135
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg
				140					145					150
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln
				155					160					165
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val
				170					175					180
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu
				185					190					195
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met
				200					205					210
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys
				215					220					225
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg
				230					235					240
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn
				245					250					255
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His
				260					265					270
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu
				275					280					285
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys
				290					295					300
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser
				305					310					315
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr
				320					325					330
Ser	Phe	Leu	Met	Ser										
				335										

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
 aagcaaccaa actgcaagct ttgggagttg ttcgctgtcc ctgccctgct 50
 ctgctaggga gagaacgcca gagggaggcg gctggcccgg cggcaggctc 100

tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
atggatggat gtcattggaga ggcatggcta ccgaacacag aaatttgagg 500
aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggg 600
taatcttacc cgtaacagga ctaaagtcag agtgatggaa agggattggc 650
agaatacaga caaagcagta aactgggtta gaaaggaagc aattaattac 700
actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750
ttcaccatct tctggagaaa attttgatc ttcaacatct cacacatctc 800
tttattggct tgaaaaagtg tctcatgatg ccatcaaat cccaaagtgg 850
tcacctttgt cagaaatgca ccctgtagat tattactctt cttatacaaa 900
aaactgcact ggaagattta caaaaaaga aattaagaat attagagcat 950
tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000
ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050
ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100
gcatgtacga ggctagtga catgttccgc ttttgatgat gggaccagga 1150
attaaagccg gcctacaagt atcaaatgtg gtttctcttg tggatattta 1200
ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagt 1250
gatactcttt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300
gtcaaaaacc tgcatccacc ctggattctg agtgaattcc atggatgtaa 1350
tgtgaatgcc tccacctaca tgcttcgaac taacctgagc aaatatatag 1400
cctattcgga tgggtgcatc atattgcctc aactctttga tctttcctcg 1450
gatccagatg aattaacaaa tgttgctgta aaatttccag aaattactta 1500
ttctttggat cagaagcttc attcattat aaactaccct aaagtttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600
 ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650
 ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700
 aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagt 1750
 ttctagagat acatataaat atattacaag atcataatta tgtattttta 1800
 atgaaacagt ttttaataatt accaagtttt ggccggggcac agtgggtcac 1850
 acctgtaatc ccaggacttt gggagggtga ggaaagcaga tcacaagggtc 1900
 aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950
 aaatacaaaa attagctggg cgcgggtggtg cacacctata gtctcagcta 2000
 ctcagagggt gaggcaggag gatcgcttga acccgggagg cagcagttgc 2050
 agtgagctga gattgcgcca ctgtactcca gcctggcaac agagtgagac 2100
 tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150
 tattttgtaa gaatgtagtg tattttaaga taaaatgcc aatgattataa 2200
 aatcacatat tttcaaaaat gggtattatt taggcctttg tacaatttct 2250
 aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300
 atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
 taaaatagtt gtatgtgagc atttgatggt gaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2450
 aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132
 Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala
 1 5 10 15
 Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
 20 25 30
 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
 35 40 45
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
 50 55 60
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
 65 70 75

[illegible]

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys		
380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser		
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg		
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile		
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr		
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln		
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val		
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile		
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln		
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln		
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val		
530	535	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
 gagagaagtc agcctggcag agagactctg aaatgaggga ttagaggtgt 50
 tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100
 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150
 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
 catcaccagc tgtgacatct atagaccctt tctgggcctg cccgctgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgcgat ctccctccctg 400
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atccccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatac 550
 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650
 ctggaatcat cctctgcttt tctgtctcat cccagagaaa tcgctccaac 700
 tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750
 gcctgggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
 cagggtatgt gtgaagaacc aggggccaga gctgggggggt ggctgggtct 850
 gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900
 actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950
 ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000
 attgccaaag atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050
 gctcccctgc cctaagtccc caacctcaa cttgaaaccc cattccctta 1100
 agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150
 ccccaaaccc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200
 ccctctctct ggctgagggtt ggctcttagc tcattgctgg ggatgggaag 1250
 gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300
 cctccaaaga aactgattgg ccttgaacc tccatcccac tcttgttatg 1350
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
 tacggtatcc agggaaacaga aagcaggatg caggatggga ggacaggaag 1450
 gcagcctggg acatttaaaa aaata 1475

<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 1 5 10 15
 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
 20 25 30
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

atctcccatc tccagtaaact gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
 1 5 10 15
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
 ctccactgca accaccaga gccatggctc cccgaggctg catcgtagct 50
 gtctttgcca ttttctgcat ctccaggctc ctctgtctac acggagcccc 100
 agtggtcccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtctgcc cctggacctt catggtgaag ctgataaacc 300
 agaactgcga ctcagcccg accctggatg acaggctttg tcgcagtgtc 350
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400
 tgggccttga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
 ggactctgaa cctcctgat gaccctatg gccaacatca acccggcacc 650
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
 tatgtacttt ataatgaaa a 771

<210> 138
 <211> 110
 <212> PRT
 <213> Homo sapiens.

<400> 138
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
 1 5 10 15
 Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met
 20 25 30
 Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
 35 40 45
 Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
 50 55 60
 Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
 65 70 75
 Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
 80 85 90
 Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
 95 100 105
 Cys Arg Ser Val Ser
 110

<210> 139
 <211> 2044
 <212> DNA
 <213> Homo sapiens

<400> 139

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 gctcgcaactc agtcgcggga ggcttccccg cgccggccgc gtcccgcccc 100
 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgctc 150
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200
 tctcttccctg gctgcgtccc taggtccggg ggcagccttc aaggctcgcca 250
 cgccgtatcc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300
 tgcaggctct tgggccctgt ggacaaagg cagcatgtga ccttctacaa 350
 gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400
 ggcccatccg caacctcag ttccaggacc ttacctgca ccatggaggc 450
 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
 ccctgctgga tagcggcctc tactgctgcc tgggtggtgga gatcaggcac 600
 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650
 aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700
 atagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750
 ggaatcctct gcctccccct catcctgctc ctggtctaca agcaaaggca 800
 ggcagcctcc aaccgccgtg ccaggagct ggtgcggatg gacagcaaca 850
 ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900
 ataccgagg ccaaagtcag gcacccctg tcctatgtgg ccagcgga 950
 gccttctgag tctggggcgc atctgcttcc ggagccagc acccccctgt 1000
 ctctccagg ccccgagac gtcttcttcc catccctgga ccctgtccct 1050
 gactctcaa actttgaggt catctagccc agctggggga cagtgggctg 1100
 ttgtggctgg gtctggggca ggtgcatttg agccagggt ggctctgtga 1150
 gtggcctcct tggcctcggc cctggttccc tccctcctgc tctgggctca 1200
 gatactgtga catcccagaa gccagcccc tcaacctc tggatgctac 1250
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 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

tgggccaccc tcccaggcac cagacacagg gcacgggtgga gagacttctc 1500
 ccccggtggcc gccttggctc ccccgttttg cccgaggctg ctcttctgtc 1550
 agacttcctc tttgtaccac agtggctctg gggccaggcc tgcctgcca 1600
 ctggccatcg ccaccttccc cagctgcctc ctaccagcag tttctctgaa 1650
 gatctgtcaa caggttaagt caatctgggg cttccactgc ctgcattcca 1700
 gtccccagag cttggtggtc ccgaaacggg aagtacatat tggggcatgg 1750
 tggcctccgt gagcaaattg tgtcttgggc aatctgaggc caggacagat 1800
 gttgccccac ccactggaga tgggtgctgag ggaggtgggt ggggccttct 1850
 gggaaggtga gtggagaggg gcacctgccc cccgccctcc ccattccccta 1900
 ctccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 140
 Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly
 1 5 10 15
 Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
 20 25 30
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
 35 40 45
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
 50 55 60
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
 65 70 75
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
 80 85 90
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
 95 100 105
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
 110 115 120
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
 125 130 135
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

Ile Arg His His	His Ser Glu His Arg	Val His Gly Ala Met	Glu
	155	160	165
Leu Gln Val Gln	Thr Gly Lys Asp Ala	Pro Ser Asn Cys Val	Val
	170	175	180
Tyr Pro Ser Ser	Ser Gln Asp Ser Glu	Asn Ile Thr Ala Ala	Ala
	185	190	195
Leu Ala Thr Gly	Ala Cys Ile Val Gly	Ile Leu Cys Leu Pro	Leu
	200	205	210
Ile Leu Leu Leu	Val Tyr Lys Gln Arg	Gln Ala Ala Ser Asn	Arg
	215	220	225
Arg Ala Gln Glu	Leu Val Arg Met Asp	Ser Asn Ile Gln Gly	Ile
	230	235	240
Glu Asn Pro Gly	Phe Glu Ala Ser Pro	Pro Ala Gln Gly Ile	Pro
	245	250	255
Glu Ala Lys Val	Arg His Pro Leu Ser	Tyr Val Ala Gln Arg	Gln
	260	265	270
Pro Ser Glu Ser	Gly Arg His Leu Leu	Ser Glu Pro Ser Thr	Pro
	275	280	285
Leu Ser Pro Pro	Gly Pro Gly Asp Val	Phe Phe Pro Ser Leu	Asp
	290	295	300
Pro Val Pro Asp	Ser Pro Asn Phe Glu	Val Ile	
	305	310	

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
 cccacgcgtc cgcgctctc ccttctgctg gaccttcctt cgtctctcca 50
 tctctccctc ctttccccgc gttctctttc cacctttctc ttcttccac 100
 cttagacctc ctttctgcc ctcttttctt gccacccgct gcttcttggc 150
 ctttctccga ccccgctcta gcagcagacc tcctgggggc tgtgggttga 200
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctcccgg accagcggcc tgacctggg gaaaggatgg ttcccgaggt 300
 gaggtcctc tcctccttgc tgggactcgc gctgctctgg ttccccctgg 350
 actccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400
 agatactccc ccggcgagag ctggcaccct tacttgagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttggt 500
 accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
 cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
 ggccccacca aagtcctgcc agcacaacgg gaccatgta' caacacggag 650
 agatcttcag tgcccatgag ctgttccct cccgcctgcc caaccagtgt 700
 gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
 ccccgaaacca ggctgcccag caccctccc actgccagac tctgctgcc 800
 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
 cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
 tgggagaaag agaggcccg gcacccagc cccactggc ctcagcgccc 950
 ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
 actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
 cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100
 tcggccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150
 tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200
 agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250
 gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
 ctcgccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350
 cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400
 taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
 ccacacagcc agaattctcc acttgactca gatcaagaaa gtcaggaagc 1500
 aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
 gaaggctact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
 gatatgagct gtataattgt tggtattata tattaataaa taagaagttg 1700
 cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
 <211> 451
 <212> PRT
 <213> Homo sapiens
 <400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala
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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp
				20					25					30
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser
				35					40					45
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg
				50					55					60
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His
				65					70					75
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln
				80					85					90
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg
				95					100					105
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His
				110					115					120
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro
				125					130					135
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys
				140					145					150
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro
				155					160					165
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu
				170					175					180
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg
				185					190					195
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly
				200					205					210
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe
				215					220					225
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val
				230					235					240
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly
				245					250					255
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg
				260					265					270
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly
				275					280					285
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys

	290		295		300
Arg His Pro Glu	Lys Val Ala Gly Lys	Cys Cys Lys Ile Cys	Pro		
	305		310		315
Glu Asp Lys Ala	Asp Pro Gly His Ser	Glu Ile Ser Ser Thr	Arg		
	320		325		330
Cys Pro Lys Ala	Pro Gly Arg Val Leu	Val His Thr Ser Val	Ser		
	335		340		345
Pro Ser Pro Asp	Asn Leu Arg Arg Phe	Ala Leu Glu His Glu	Ala		
	350		355		360
Ser Asp Leu Val	Glu Ile Tyr Leu Trp	Lys Leu Val Lys Asp	Glu		
	365		370		375
Glu Thr Glu Ala	Gln Arg Gly Glu Val	Pro Gly Pro Arg Pro	His		
	380		385		390
Ser Gln Asn Leu	Pro Leu Asp Ser Asp	Gln Glu Ser Gln Glu	Ala		
	395		400		405
Arg Leu Pro Glu	Arg Gly Thr Ala Leu	Pro Thr Ala Arg Trp	Pro		
	410		415		420
Pro Arg Arg Ser	Leu Glu Arg Leu Pro	Ser Pro Asp Pro Gly	Ala		
	425		430		435
Glu Gly His Gly	Gln Ser Arg Gln Ser	Asp Gln Asp Ile Thr	Lys		
	440		445		450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
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 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150
 tgggctacgc gtcctcgtt atcgtgaccc cgaggagagcg gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctcc gtgggcgccg 400
 gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccgggggtcct 500
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaagggtcc gcaaggcggg ccaggggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaaa tcatgtttcct ccaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100
 caggctgccca tggggcccag caccctctc ctcatcttgt tcctttttgtc 150
 atggtcggga cccctccaag gacagcagca ccaccttggtg gactacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgctctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
 tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500
 tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
 ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600
 gcaaacagag aagatctacg tgtttagatgg gacacagaat gacacagcct 650
 ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccggaaa 700
 gcttcccagag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750
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 aaccgaacag tgggtggacag ctcaagtatt ccagcagagg ggctgatccc 900
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 aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000
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 accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100
 tctatgtcgt ctataacacc cgtcctgcc agtcgggccc catccagtgc 1150
 tcctttgatg ccagcggcac cctgaccct gaacgggcag cactccctta 1200
 ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250
 aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
 catctttctc actcccatc atttatatta tatcccact aaatttcttg 1400
 ttcctcattc ttcaaagtgt ggccagttgt ggctcaaac ctctatatatt 1450
 ttagccaatg gcaatcaaat tctttcagct cttttgtttc atacggaaact 1500
 ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550
 ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600
 cccagacca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650
 agcagtgttc ttcccctcag agtgacttgg ggagggagaa ataggaggag 1700
 acgtccagct ctgtcctctc ttcctcactc ctcccttcag tgtcctgagg 1750
 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala
260 265 270

Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala
275 280 285

Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys
290 295 300

Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro
305 310 315

Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr
320 325 330

Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile
335 340 345

Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
350 355 360

Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu
365 370 375

Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly
380 385 390

Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu
395 400 405

Val

<210> 147
<211> 2052
<212> DNA
<213> Homo sapiens

<400> 147
gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgccct 50
ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
gttctcctct tctctctaatt ccatccgtca cctctcctgt catccgtttc 150
catgccgtga ggtccattca cagaacacat ccatggtctt catgctcagt 200
ttgggttctga gtctcctcaa gctgggatca gggcagtgga aggtgttttg 250
gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300
gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
attctattgc ggaggggacg atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtc 650
 tcgggctggt tccccggcc cacagcgaag tggaaaggtc cacaaggaca 700
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg 750
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagat 850
 aggagatacc ttttctgagc ctatatcgtg gcacctggct accaaagtac 900
 tgggaatact ctgctgtggc ctattttttg gcattgttgg actgaagatt 950
 ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000
 aaagcacgga caggcagaat tgagagacgc ccggaaacac gcagtggagg 1050
 tgactctgga tccagagacg gctcaccgga agctctgcgt ttctgatctg 1100
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200
 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250
 gtgtgccggg atgatgtgga caggaggaag gactacgtga ctttgtctcc 1300
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
 cattaaatcc ccgttttctc agcgtcttcc ccaggacccc acctacaaaa 1400
 ataggggtct tcttgacta tgagtgtggg accatctcct tcttcaacat 1450
 aaatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat 1500
 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaaactccc 1550
 atagtcatct gccagtcac ccaggaatca gagaaagagg cctcttggca 1600
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tctcacagg 1650
 caaccacgcc cttctcccc aggggtgaaa tgtaggatga atcacatccc 1700
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 cattacattt agtttgcct cactccatct ggctaagtga tcttgaaata 1900
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000

acagagtgta tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050

aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly
1				5					10					15

Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala
				20					25					30

Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys
				35					40					45

Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe
				50					55					60

Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe
				65					70					75

Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp
				80					85					90

Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr
				95					100					105

Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser
				110					115					120

Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly
				125					130					135

Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile
				140					145					150

Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala
				155					160					165

Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg
				170					175					180

Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu
				185					190					195

Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His
				200					205					210

Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp
				215					220					225

Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys	
245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcggcg gcggttgccg aggettcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cgggtggcggc ggggccgcgg ggcaggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggccc ccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

cacccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcgcccc ctgcgcgacc acccctcccg cggcggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgcgcgcg accacccttt cgacgaccac 550
tggccccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600
ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650
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agaccacagg gcagtgtgag tgtcggccag gttatcaggg gcttcaactgt 800
gaaacctgca aagaggggctt ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaaaaa 950
aaaaggctgc tactctcaag gaccatactg gtttaaacaa aggaggatga 1000
gggtcataga tttacaaaat attttatata cttttattct cttactttat 1050
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100
tcttcaaaag cactagagtc gccaattttt ctctgggata atttctgtaa 1150
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ttcaggcatg aaacctgcta ggaggtttag aaatgttctt atgtttatta 1250
atataccatt ggagtttgag gaaatttggt gtttggttta tttttctctc 1300
taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350
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aactattatg ttatttgagg gtaatttaat ctagtggaat aatgtactgt 1500
tatctaagca tttgccttgt actgcactga aagtaattat tctttgacct 1550
tatgtgaggc acttggcttt ttgtggaccc caagtcaaaa aactgaagag 1600
acagtattaa ataatgaaaa aaataatgac aggttatact cagtgttaacc 1650
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ctggtttggt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcttt atacttttagc 1900
 actaaatatt ttaaagtctt tataaatgat attatactgt tatggaatat 1950
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
 ctacgcctg taatcctagc actttgggag gccaaaggcg gtggatcact 2050
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 ctactaaaaa tacaaacaaa ttagctgggc gtggtggcac acacctgtag 2150
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200
 tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250
 agaggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153
 <211> 258
 <212> PRT
 <213> Homo sapiens

<400> 153
 Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys
 1 5 10 15
 Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn
 20 25 30
 Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro
 35 40 45
 Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala
 50 55 60
 Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
 65 70 75
 Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
 80 85 90
 Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
 95 100 105
 Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
 110 115 120
 Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
 125 130 135
 Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
 140 145 150
 Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
 155 160 165
 Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
 tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
 ttctggcttt ggtctcgggtg cccagggccc aggcctgtgtg gttgggaaga 100
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtaggcctc 150
 ccgggaaaag ggctttgccca tggagaagga catgaagaac gtcgtggggg 200
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tgctggccac caacttcaga gactatgccca tcattctcac tcagctggag 400
 ttccggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttctctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600
 gggctcctgtg acctcggcca gtgtccaccc acctcgtca gcggctcccg 650
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
 95 100 105
 Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
 110 115 120
 Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
 125 130 135
 Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
 140 145 150
 Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
 155 160

<210> 159
 <211> 1665
 <212> DNA
 <213> Homo sapiens

<400> 159
 aacagacggt cctcgcggc cctggcacct ctaaccccag acatgctgct 50
 gctgctgctg cccctgctct gggggaggga gagggcgga ggacagacaa 100
 gtaaactgct gacgatgcag agttccgtga cggatgcagga aggcctgtgt 150
 gtccatgtgc cctgctcctt ctccacccc tcgcatggct ggatttacct 200
 tggcccagta gttcatggct actggttccg ggaaggggac aatacagacc 250
 aggatgctcc agtggccaca aacaacccag ctccgggcagt gtgggaggag 300
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
 cctgagcatc agagatgcc aagaagtga tgcggggaga tacttctttc 400
 gtatggagaa aggaagtata aatggaatt ataaacatca ccggctctct 450
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
 cctggagtcc ggctgcccc agaactctgac ctgctctgtg ccctgggcct 550
 gtgagcaggg gacacccct atgatctcct ggatagggac ctccgtgtcc 600
 cccctggacc cctccaccac ccgctcctcg gtgctcacc tcacccaca 650
 gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
 ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgccc 850
 tggctctgtg agttgatgca gttgacagca atccccctgc caggctgagc 900
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950

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<210> 160
<211> 463
<212> PRT
<213> Homo sapiens
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166

Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu	110	115	120
125 130 135			
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile	140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser	155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp	170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
 410 415 420
 Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
 425 430 435
 Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
 440 445 450
 Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
 455 460

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gctcggcctg gccgctgcc tgtccttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttcggag gacaggaggc ccaggaaggt gtccccagtg 200
 aaggtgacag ccctgggagg tgggaagttg gaagccacgt tcaccttcat 250
 gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcca ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttcctt 650
 gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20					25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg
			35					40					45	
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly
			50					55					60	
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile
			65					70					75	
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr
			80					85					90	
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro
			95					100					105	
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly
			110					115					120	
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr
			125					130					135	
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys
			140					145					150	
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser
			155					160					165	
Cys	Val	Pro	Glu	His										
			170											

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
caggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatatc acaggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50
cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtga agcctcactc 200
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250
cgacgtcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccggacag ccactgagtc cttccccac cccggcttca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500
ctcacgtgtg gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600
atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
attatctcct ggggccagga tccgtgtgcg atcaccggaa agcctggtgt 800
ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850
acaattagac tggaccacc caccacagcc catcaccctc catttccact 900
tgggtgtttg ttctgttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattctttg gctcctgga ctacaggaga tgctgtcact 1000
taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050
ccttgaaata ttgtgactct gggaatgaca acacctggtt tggttctctgt 1100
tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
1 5 10 15

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	
				20					25					30	
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	
				35					40					45	
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	
				50					55					60	
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	
				65					70					75	
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	
				80					85					90	
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	
				95					100					105	
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	
				110					115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	
				125					130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	
				140					145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	
				155					160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	
				170					175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	
				185					190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	
				200					205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	
				215					220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	
				230					235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
				245					250						

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171
ggctgcgggga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc gggcg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 176
 cccttgatga tcctgggc 18

<210> 177
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 177
 aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggcctt 50

<210> 178
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 178
 gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179
 <211> 907
 <212> DNA
 <213> Homo sapiens

<400> 179
 gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50
 gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100
 aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150
 agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgccatt 200
 atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250
 caaaatgaag gccaccccaa atgggttggt cttgggtgtg ggcaagtcac 300
 aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350
 aagtagttat acccccttca ttgcatatcg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
 tgtgacaaaa ggaccacgga gcattgagac atttaaacia atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
 atttctactt ttttttttta gctatttact gtactttatg tataaaacia 750
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctggt 850
 ttgcaaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
 1 5 10 15
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
 20 25 30
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
 35 40 45
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
 50 55 60
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
 65 70 75
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
 80 85 90
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
 95 100 105
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
 110 115 120
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
 125 130 135
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
 140 145 150

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu
155 160 165
Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys
170 175 180
Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu
185 190 195
Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser
200 205 210
Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu
215 220

<210> 181
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-22
<223> Synthetic construct.

<400> 181
gtgttctgct ggagccgatg cc 22

<210> 182
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 182
gacatggaca atgacagg 18

<210> 183
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 183
cctttcagga tgtaggag 18

<210> 184
<211> 18
<212> DNA
<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 184
 gatgtctgcc accccaag 18

 <210> 185
 <211> 27
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

 <400> 185
 gcatcctgat atgacttgct acgtggc 27

 <210> 186
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 186
 tacaagaggg aagaggagtt gcac 24

 <210> 187
 <211> 52
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-52
 <223> Synthetic construct.

 <400> 187
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

 cc 52

 <210> 188
 <211> 573
 <212> DNA
 <213> Homo sapiens

 <400> 188
 cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50

 ctctttggag ctgtgactca gaaaaccaa acttcctgtg ctaagtgcc 100

atactttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200
 aacgccaggc atgggtggctc ggcctgttaa tcccagttct ttgggaagcc 250
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
 ttcttgtttc atttcgcgac tgccctctca gtgtttcttg ggatcccctc 550
 ccaaataaag tacttatatt ctc 573

<210> 189
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 189
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
 1 5 10 15
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
 65 70

<210> 190
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 190
 aggaccatt gcttcttcca ggcc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 191
 cgttacatgt ctccaagggg aatg 24

<210> 192
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 192
 cctgtgctaa gtgccccca aatgcttct gtgtcaataa cactcactgc 50

<210> 193
 <211> 1091
 <212> DNA
 <213> Homo sapiens

<400> 193
 caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
 ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100
 gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150
 gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
 gtgtgggctg aactcacagc cgtggcaggc ggggctgttt gagggcacca 250
 gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
 gctcactgca gcggcagcag gtactgggtg cgcctggggg aacacagcct 350
 cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
 cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
 ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccctt 500
 gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550
 gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600
 tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
 cgggagaatc acgagcaaca tgggtgtgtg aggcggcgtc ccggggcagg 700
 atgcctgcca gggtgattct gggggcccc tgggtgtgtg gggagtcctt 750
 caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

200	205	210
Gln Gly Leu Val Ser Trp Gly Ser Val	Gly Pro Cys Gly Gln Asp	
215	220	225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile	Cys Lys Tyr Val Asp Trp	
230	235	240
Ile Arg Met Ile Met Arg Asn Asn		
245		

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
 gcggccacac gcagctagcc ggagcccgga ccaggcgcct gtgcctcctc 50
 ctcgtccctc gccgcgtccg cgaagcctgg agccggcgagg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccacac ctggagatga agaagatgat ctacagagggt acaggagggg 400
 tcagtgcacac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
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 <212> PRT
 <213> Homo sapiens

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 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
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 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
 95 100 105
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
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<400> 197

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[illegible]

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<211> 1523
<212> PRT
<213> Homo sapiens
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Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	
				35					40					45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	
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Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	
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Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	
				80					85					90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	
				95					100					105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	
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Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	
				125					130					135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	
				140					145					150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	
				155					160					165	

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175	180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Ile Ser Arg	185	190	195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205	210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220	225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235	240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250	255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr	320	325	330
Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp	335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu	350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe	365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys	380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu	395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys	410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala	425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp	440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser			

455					460					465				
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser
				470					475					480
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe
				485					490					495
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg
				500					505					510
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg
				515					520					525
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn
				530					535					540
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys
				545					550					555
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys
				560					565					570
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu
				575					580					585
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val
				590					595					600
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn
				605					610					615
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser
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Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr
				635					640					645
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu
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Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly
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Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys
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Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala
				695					700					705
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln
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Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val
				725					730					735
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met
				740					745					750

Pro Lys Asp Val	Thr Glu Leu Tyr Leu	Glu Gly Asn His Leu Thr	755	760	765
Ala Val Pro Arg	Glu Leu Ser Ala Leu	Arg His Leu Thr Leu Ile	770	775	780
Asp Leu Ser Asn	Asn Ser Ile Ser Met	Leu Thr Asn Tyr Thr Phe	785	790	795
Ser Asn Met Ser	His Leu Ser Thr Leu	Ile Leu Ser Tyr Asn Arg	800	805	810
Leu Arg Cys Ile	Pro Val His Ala Phe	Asn Gly Leu Arg Ser Leu	815	820	825
Arg Val Leu Thr	Leu His Gly Asn Asp	Ile Ser Ser Val Pro Glu	830	835	840
Gly Ser Phe Asn	Asp Leu Thr Ser Leu	Ser His Leu Ala Leu Gly	845	850	855
Thr Asn Pro Leu	His Cys Asp Cys Ser	Leu Arg Trp Leu Ser Glu	860	865	870
Trp Val Lys Ala	Gly Tyr Lys Glu Pro	Gly Ile Ala Arg Cys Ser	875	880	885
Ser Pro Glu Pro	Met Ala Asp Arg Leu	Leu Leu Thr Thr Pro Thr	890	895	900
His Arg Phe Gln	Cys Lys Gly Pro Val	Asp Ile Asn Ile Val Ala	905	910	915
Lys Cys Asn Ala	Cys Leu Ser Ser Pro	Cys Lys Asn Asn Gly Thr	920	925	930
Cys Thr Gln Asp	Pro Val Glu Leu Tyr	Arg Cys Ala Cys Pro Tyr	935	940	945
Ser Tyr Lys Gly	Lys Asp Cys Thr Val	Pro Ile Asn Thr Cys Ile	950	955	960
Gln Asn Pro Cys	Gln His Gly Gly Thr	Cys His Leu Ser Asp Ser	965	970	975
His Lys Asp Gly	Phe Ser Cys Ser Cys	Pro Leu Gly Phe Glu Gly	980	985	990
Gln Arg Cys Glu	Ile Asn Pro Asp Asp	Cys Glu Asp Asn Asp Cys	995	1000	1005
Glu Asn Asn Ala	Thr Cys Val Asp Gly	Ile Asn Asn Tyr Val Cys	1010	1015	1020
Ile Cys Pro Pro	Asn Tyr Thr Gly Glu	Leu Cys Asp Glu Val Ile	1025	1030	1035
Asp His Cys Val	Pro Glu Leu Asn Leu	Cys Gln His Glu Ala Lys			

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Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
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Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
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His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
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Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
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His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
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Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
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Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
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Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
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Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
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Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
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Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
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Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
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Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
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Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
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Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
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Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
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 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
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 1370 1375 1380
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
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 1400 1405 1410
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
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 <213> Artificial

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 <223> Synthetic construct.

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<220>

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<223> Synthetic construct.

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gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
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 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctcgagggt ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
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ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
gaggaatata ccacagggcat ggcagactgc atcttagtca acagccagtt 350
cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
ctgatgtcct ctatccatct cttaaagtca ccagctttga ctcagttgtt 450
cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
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tgtccctctg gaagccatgt acatgcagtg ccagtcatt gctgttaatt 850
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tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400
atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450
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tcaactgtcat ctgttaggga atttttgttt gtccctgtct tgcctggatc 1550
catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600
actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210
<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	260	265	270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
 275 280 285
 Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
 290 295 300
 Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
 305 310 315
 Arg Tyr Val Thr Lys Leu Leu Val
 320

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
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 cttcgcgata ttccgcgtta ccttcttgct ggcgttgggt ggagccgtgc 100
 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgggaa 200
 tttgcatgag ttctctggtta atttgcata gagatatggg cctgtggtct 250
 ccttctggtt tggcaggcgc ctcgtggtta gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg ctccagaag aatcatggca cagtttggtc 650
 tgagattgga aaaggcttct tagatgggtc acttgataaa aacatgactc 700
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
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 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

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gccaaactga	ctccagtttc	tgcccagctt	caagatattg	aaggaaaaat	1100
tgaccgattt	attattccta	gagagaccct	cgtcctttat	gcccttggtg	1150
tggtacttca	ggatccta	acttggccat	ctccacaca	gtttgatcca	1200
gatcggtttg	atgatgaatt	agtaatgaaa	actttttcct	cacttggatt	1250
ctcaggcaca	caggagtgtc	cagagttgag	gtttgcatat	atgggtgacca	1300
cagtacttct	tagtgtattg	gtgaagagac	tgcacctact	ttctgtggag	1350
ggacagggtta	ttgaaacaaa	gtatgaactg	gtaacatcat	caaggggaaga	1400
agcttggatc	actgtctcaa	agagatatta	aaattttata	cattttaa	1450
cattgttaaa	ttgattgagg	aaaacaacca	tttaaaaaaa	atctatgttg	1500
aatcctttta	taaaccagta	tcactttgta	atataaacac	ctatttgtac	1550
ttaa	1554				

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<210> 212
<211> 462
<212> PRT
<213> Homo sapiens
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<400> 212
Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
  1          5          10          15
Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
          20          25          30
Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
          35          40          45
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
          50          55          60
Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
          65          70          75
Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
          80          85          90
Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
          95          100          105
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
          110          115          120
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
          125          130          135
Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

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Asp Lys Trp Leu	Ser Tyr Pro Glu Thr	Gln His Val Pro Leu	Ser
	155	160	165
Gln His Met Leu	Gly Phe Ala Met Lys	Ser Val Thr Gln Met	Val
	170	175	180
Met Gly Ser Thr	Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe	Gln
	185	190	195
Lys Asn His Gly	Thr Val Trp Ser Glu	Ile Gly Lys Gly Phe	Leu
	200	205	210
Asp Gly Ser Leu	Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr	Glu
	215	220	225
Asp Ala Leu Met	Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile	Lys
	230	235	240
Glu Arg Lys Gly	Arg Asn Phe Ser Gln	His Ile Phe Ile Asp	Ser
	245	250	255
Leu Val Gln Gly	Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp	Ser
	260	265	270
Met Ile Phe Ser	Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu	Cys
	275	280	285
Thr Trp Ala Ile	Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln	Lys
	290	295	300
Lys Leu Tyr Glu	Glu Ile Asn Gln Val	Phe Gly Asn Gly Pro	Val
	305	310	315
Thr Pro Glu Lys	Ile Glu Gln Leu Arg	Tyr Cys Gln His Val	Leu
	320	325	330
Cys Glu Thr Val	Arg Thr Ala Lys Leu	Thr Pro Val Ser Ala	Gln
	335	340	345
Leu Gln Asp Ile	Glu Gly Lys Ile Asp	Arg Phe Ile Ile Pro	Arg
	350	355	360
Glu Thr Leu Val	Leu Tyr Ala Leu Gly	Val Val Leu Gln Asp	Pro
	365	370	375
Asn Thr Trp Pro	Ser Pro His Lys Phe	Asp Pro Asp Arg Phe	Asp
	380	385	390
Asp Glu Leu Val	Met Lys Thr Phe Ser	Ser Leu Gly Phe Ser	Gly
	395	400	405
Thr Gln Glu Cys	Pro Glu Leu Arg Phe	Ala Tyr Met Val Thr	Thr
	410	415	420
Val Leu Leu Ser	Val Leu Val Lys Arg	Leu His Leu Leu Ser	Val
	425	430	435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
455 460

<210> 213
<211> 759
<212> DNA
<213> Homo sapiens

<400> 213
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tcagggtctg tgccctctcg ctctctgacg ctctggcgc atctggtggt 150
cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
gccgcgtct ctgtcacctt gggcctcttt gcagtggagc tggccggttt 300
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
gggctcactg tagtgcattc gtggccctgt ccttcttcat attcgagcgt 400
tgaggagtgc ctacgtattg gtacattttt gtctcttgca gtgcccttcc 450
agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
aaccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
ttccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
tgttttgtag taacattaag acttatatac agtttttaggg gacaattaaa 750
aaaaaaaaa 759

<210> 214
<211> 140
<212> PRT
<213> Homo sapiens

<400> 214
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
1 5 10 15
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
140

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
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gaccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150
ggcatcagag tgcgccagc acctgagcct gcccttacgc tatgtggtgg 200
tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctgggtgga 300
cgtgggctac aacttctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc agggcttact ggctgcgggt gtggctcagg 500
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
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catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
<211> 196
<212> PRT

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ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400
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aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
gaacggggcc gccggacctc gctttgcacc cagcaccag ccaagatctg 650
ctcccgagac cagctcaga gctcagccac ctggagctgc tcccagccct 700
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 aataaagctt gccccggggc a 1871

<210> 218
 <211> 252
 <212> PRT
 <213> Homo sapiens

<400> 218
 Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser
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 20 25 30
 Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
 35 40 45
 Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
 50 55 60
 Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
 65 70 75
 Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
 80 85 90
 Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
 95 100 105
 Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
 110 115 120
 Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
 125 130 135
 His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
 140 145 150
 Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
 155 160 165
 Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
 170 175 180
 Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
 185 190 195
 Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
 200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219
<211> 2065
<212> DNA
<213> Homo sapiens

<400> 219
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tcagttttca cgtgattaaa gtctaccaga gccaaactat ccagggttaac 750
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tgttactcgt gaagctgcc acaatgggtg cctgctctac ctagataaag 850
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cagtattcca cgttttcttg ctttctggtg ttccccctat aggattcaat 950
ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
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ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100

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tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150
aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200
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<210> 220
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 220

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Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
				35					40					45
Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
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Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
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Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
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Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
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Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
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Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
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<210> 221
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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 221
 acggctcacc atgggctccg 20

<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct,

<400> 222
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<210> 223
 <211> 40

<212> DNA
 <213> Artificial

<220>
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 <222> 1-40
 <223> Synthetic construct.

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<210> 224
 <211> 902
 <212> DNA
 <213> Homo sapiens

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<210> 225
 <211> 257
 <212> PRT

<213> Homo sapiens

<400> 225

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Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
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Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	
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Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	
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Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	
				80					85					90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	
				95					100					105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
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Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
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Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140					145					150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
				155					160					165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200					205					210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
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Ser Arg

<210> 226

<211> 3939
 <212> DNA
 <213> Homo sapiens

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 tacaccttca accatactgt gacccgcaac aggacagagg gcgtgctgtg 250
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<210> 227
 <211> 832
 <212> PRT
 <213> Homo sapiens

<400> 227
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 Val Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln
 20 25 30

(Musical notation for Example 6)

320										325					330				
Ile	Asp	Arg	Ala	Cys	Pro	Glu	Ser	Gly	His	Pro	Arg	Val	Leu	Ala					
				335					340					345					
Asp	Ser	Phe	Pro	Gly	Ser	Ser	Pro	Tyr	Glu	Gly	Tyr	Asn	Tyr	Gly					
				350					355					360					
Ser	Phe	Glu	Asn	Val	Ser	Gly	Ser	Thr	Asp	Gly	Leu	Val	Asp	Ser					
				365					370					375					
Ala	Gly	Thr	Gly	Asp	Leu	Ser	Tyr	Gly	Tyr	Gln	Gly	Arg	Ser	Phe					
				380					385					390					
Glu	Pro	Val	Gly	Thr	Arg	Pro	Arg	Val	Asp	Ser	Met	Ser	Ser	Val					
				395					400					405					
Glu	Glu	Asp	Asp	Tyr	Asp	Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp	Lys					
				410					415					420					
Asn	Val	Ile	Arg	Thr	Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala					
				425					430					435					
Arg	Lys	Asp	Lys	Arg	Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe					
				440					445					450					
Trp	Asn	Ile	Ala	Thr	Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val					
				455					460					465					
Gln	Leu	Val	Ile	Thr	Tyr	Gln	Thr	Val	Val	Asn	Val	Thr	Gly	Asn					
				470					475					480					
Gln	Asp	Ile	Cys	Tyr	Tyr	Asn	Phe	Leu	Cys	Ala	His	Pro	Leu	Gly					
				485					490					495					
Asn	Leu	Ser	Ala	Phe	Asn	Asn	Ile	Leu	Ser	Asn	Leu	Gly	Tyr	Ile					
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Leu	Leu	Gly	Leu	Leu	Phe	Leu	Leu	Ile	Ile	Leu	Gln	Arg	Glu	Ile					
				515					520					525					
Asn	His	Asn	Arg	Ala	Leu	Leu	Arg	Asn	Asp	Leu	Cys	Ala	Leu	Glu					
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Cys	Gly	Ile	Pro	Lys	His	Phe	Gly	Leu	Phe	Tyr	Ala	Met	Gly	Thr					
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Ala	Leu	Met	Met	Glu	Gly	Leu	Leu	Ser	Ala	Cys	Tyr	His	Val	Cys					
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Pro	Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met	Tyr	Met					
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Ile	Ala	Gly	Leu	Cys	Met	Leu	Lys	Leu	Tyr	Gln	Lys	Arg	His	Pro					
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Asp	Ile	Asn	Ala	Ser	Ala	Tyr	Ser	Ala	Tyr	Ala	Cys	Leu	Ala	Ile					
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<212> PRT

<213> Homo sapiens

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Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
1					5				10					15

Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

20					25					30				
Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro
			35					40					45	
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
			50					55					60	
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
			65					70					75	
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala
			80					85					90	
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val
			95					100					105	
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn
			110					115					120	
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu
			125					130					135	
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala
			140					145					150	
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe
			155					160					165	
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe
			170					175					180	
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly
			185					190					195	
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu
			200					205					210	
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala
			215					220					225	
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser
			230					235					240	
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro
			245					250					255	
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr
			260					265					270	
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu
			275					280					285	
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala
			290					295					300	
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp
			305					310					315	

Tyr	Ala	Ala	Pro	Leu 320	Glu	Leu	His	Val	Leu 325	Val	Met	Asp	Glu	Asn 330
Asp	Asn	Val	Pro	Ile 335	Cys	Pro	Pro	Arg	Asp 340	Pro	Thr	Val	Ser	Ile 345
Pro	Glu	Leu	Ser	Pro 350	Pro	Gly	Thr	Glu	Val 355	Thr	Arg	Leu	Ser	Ala 360
Glu	Asp	Ala	Asp	Ala 365	Pro	Gly	Ser	Pro	Asn 370	Ser	His	Val	Val	Tyr 375
Gln	Leu	Leu	Ser	Pro 380	Glu	Pro	Glu	Asp	Gly 385	Val	Glu	Gly	Arg	Ala 390
Phe	Gln	Val	Asp	Pro 395	Thr	Ser	Gly	Ser	Val 400	Thr	Leu	Gly	Val	Leu 405
Pro	Leu	Arg	Ala	Gly 410	Gln	Asn	Ile	Leu	Leu 415	Leu	Val	Leu	Ala	Met 420
Asp	Leu	Ala	Gly	Ala 425	Glu	Gly	Gly	Phe	Ser 430	Ser	Thr	Cys	Glu	Val 435
Glu	Val	Ala	Val	Thr 440	Asp	Ile	Asn	Asp	His 445	Ala	Pro	Glu	Phe	Ile 450
Thr	Ser	Gln	Ile	Gly 455	Pro	Ile	Ser	Leu	Pro 460	Glu	Asp	Val	Glu	Pro 465
Gly	Thr	Leu	Val	Ala 470	Met	Leu	Thr	Ala	Ile 475	Asp	Ala	Asp	Leu	Glu 480
Pro	Ala	Phe	Arg	Leu 485	Met	Asp	Phe	Ala	Ile 490	Glu	Arg	Gly	Asp	Thr 495
Glu	Gly	Thr	Phe	Gly 500	Leu	Asp	Trp	Glu	Pro 505	Asp	Ser	Gly	His	Val 510
Arg	Leu	Arg	Leu	Cys 515	Lys	Asn	Leu	Ser	Tyr 520	Glu	Ala	Ala	Pro	Ser 525
His	Glu	Val	Val	Val 530	Val	Val	Gln	Ser	Val 535	Ala	Lys	Leu	Val	Gly 540
Pro	Gly	Pro	Gly	Pro 545	Gly	Ala	Thr	Ala	Thr 550	Val	Thr	Val	Leu	Val 555
Glu	Arg	Val	Met	Pro 560	Pro	Pro	Lys	Leu	Asp 565	Gln	Glu	Ser	Tyr	Glu 570
Ala	Ser	Val	Pro	Ile 575	Ser	Ala	Pro	Ala	Gly 580	Ser	Phe	Leu	Leu	Thr 585
Ile	Gln	Pro	Ser	Asp 590	Pro	Ile	Ser	Arg	Thr 595	Leu	Arg	Phe	Ser	Leu 600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly

605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly Asp	
620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr Leu	
635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp His	
650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala Ser	
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr Val	
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Gln Arg Asp Trp Arg Leu Gln Thr Leu	Asn Gly Ser His Ala Tyr	
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu	Pro Arg Glu His Ile Ile	
710	715	720
Pro Val Val Val Ser His Asn Ala Gln	Met Trp Gln Leu Leu Val	
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val	Glu Gly Gln Cys Met Arg	
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro	Thr Lys Leu Ser Ala Val	
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu Ile	
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Leu Ile Phe Thr His Trp Thr Met Ser	Arg Lys Lys Asp Pro Asp	
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Gln Pro Ala Asp Ser Val Pro Leu Lys	Ala Thr Val	
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 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 230
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<210> 231
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Artificial Sequence
 <222> full
 <223> Synthetic oligonucleotide probe

<400> 231
 cctgagctgt aaccccactc cagg 24

<210> 232
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 232
 agagtctgtc ccagctatct tgt 23

<210> 233
 <211> 2786
 <212> DNA
 <213> Homo sapiens

<400> 233
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 cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
 acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
 gatgtcctgg tcccatctgt cagtctgcag gcatttaa at ccttcctgag 250
 atcccagggc ttagagtacg cagtgcacat tgaggacctg caggcccttt 300
 tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
 agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
 cgagatggac aacattgccg cagactttcc tgacctggcg aggagggtga 450
 agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
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tgtgtgtgtg	tgtgtgtgtg	tgtgtgtgtt	tgtgtgtgtg	tgtctgtcta	2550
ttttgtatcc	tggaccacaa	gttcctaagt	agagcaagaa	ttcatcaacc	2600
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tgttgttgtt	ttgtttttgt	ttttttgctt	ttaccaaaca	tgtctgtaaa	2700
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<210> 234
<211> 421
<212> PRT
<213> Homo sapiens
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<400> 234														
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Cys	Gly	Gln	Glu	Lys 20	Phe	Phe	Gly	Asp	Gln 25	Val	Leu	Arg	Ile	Asn 30
Val	Arg	Asn	Gly	Asp 35	Glu	Ile	Ser	Lys	Leu 40	Ser	Gln	Leu	Val	Asn 45
Ser	Asn	Asn	Leu	Lys 50	Leu	Asn	Phe	Trp	Lys 55	Ser	Pro	Ser	Ser	Phe 60
Asn	Arg	Pro	Val	Asp 65	Val	Leu	Val	Pro	Ser 70	Val	Ser	Leu	Gln	Ala 75
Phe	Lys	Ser	Phe	Leu 80	Arg	Ser	Gln	Gly	Leu 85	Glu	Tyr	Ala	Val	Thr 90
Ile	Glu	Asp	Leu	Gln 95	Ala	Leu	Leu	Asp	Asn 100	Glu	Asp	Asp	Glu	Met 105
Gln	His	Asn	Glu	Gly 110	Gln	Glu	Arg	Ser	Ser 115	Asn	Asn	Phe	Asn	Tyr 120
Gly	Ala	Tyr	His	Ser 125	Leu	Glu	Ala	Ile	Tyr 130	His	Glu	Met	Asp	Asn 135
Ile	Ala	Ala	Asp	Phe 140	Pro	Asp	Leu	Ala	Arg 145	Arg	Val	Lys	Ile	Gly 150
His	Ser	Phe	Glu	Asn 155	Arg	Pro	Met	Tyr	Val 160	Leu	Lys	Phe	Ser	Thr 165

Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile
170 175 180

His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala
185 190 195

Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser
200 205 210

Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro
215 220 225

Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys
230 235 240

Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro
245 250 255

Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp
260 265 270

Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu
275 280 285

Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn
290 295 300

Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met
305 310 315

Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu
320 325 330

Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val
335 340 345

Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr
350 355 360

Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile
365 370 375

Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly
380 385 390

Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr
395 400 405

Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu
410 415 420

Tyr

<210> 235
<211> 1743
<212> DNA
<213> Homo sapiens

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 cccagtcag tgcccttttc cacaaattct cccaggtaac tagcttcatg 1550
 ggatgttgct ggggttaccat atttccattc cttggggctc ccaggaatgg 1600
 aaatacgcca acccagggtta ggcacctcta ttgcagaatt acaataaacac 1650
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236
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 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

200										205					210				
Lys	Trp	Glu	Lys	Pro	Phe	His	Leu	Glu	Tyr	Thr	Arg	Lys	Asn	Phe					
				215					220					225					
Pro	Phe	Leu	Val	Gly	Glu	Gln	Val	Thr	Val	Gln	Val	Pro	Met	Met					
				230					235					240					
His	Gln	Lys	Glu	Gln	Phe	Ala	Phe	Gly	Val	Asp	Thr	Glu	Leu	Asn					
				245					250					255					
Cys	Phe	Val	Leu	Gln	Met	Asp	Tyr	Lys	Gly	Asp	Ala	Val	Ala	Phe					
				260					265					270					
Phe	Val	Leu	Pro	Ser	Lys	Gly	Lys	Met	Arg	Gln	Leu	Glu	Gln	Ala					
				275					280					285					
Leu	Ser	Ala	Arg	Thr	Leu	Ile	Lys	Trp	Ser	His	Ser	Leu	Gln	Lys					
				290					295					300					
Arg	Trp	Ile	Glu	Val	Phe	Ile	Pro	Arg	Phe	Ser	Ile	Ser	Ala	Ser					
				305					310					315					
Tyr	Asn	Leu	Glu	Thr	Ile	Leu	Pro	Lys	Met	Gly	Ile	Gln	Asn	Ala					
				320					325					330					
Phe	Asp	Lys	Asn	Ala	Asp	Phe	Ser	Gly	Ile	Ala	Lys	Arg	Asp	Ser					
				335					340					345					
Leu	Gln	Val	Ser	Lys	Ala	Thr	His	Lys	Ala	Val	Leu	Asp	Val	Ser					
				350					355					360					
Glu	Glu	Gly	Thr	Glu	Ala	Thr	Ala	Ala	Thr	Thr	Thr	Lys	Phe	Ile					
				365					370					375					
Val	Arg	Ser	Lys	Asp	Gly	Pro	Ser	Tyr	Phe	Thr	Val	Ser	Phe	Asn					
				380					385					390					
Arg	Thr	Phe	Leu	Met	Met	Ile	Thr	Asn	Lys	Ala	Thr	Asp	Gly	Ile					
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Leu	Phe	Leu	Gly	Lys	Val	Glu	Asn	Pro	Thr	Lys	Ser								
				410					415										

<210> 237
 <211> 23
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

 <400> 237
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 <210> 238

<211> 47
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

 <400> 238
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 <210> 239
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 239
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 <210> 240
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 240
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 <210> 241
 <211> 48
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

 <400> 241
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 <210> 242
 <211> 2436
 <212> DNA
 <213> Homo sapiens

 <400> 242
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 agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc 2050
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 aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250
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 gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350
 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243
 <211> 596
 <212> PRT
 <213> Homo sapiens

<400> 243
 Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu
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 20 25 30
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
 35 40 45
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
 50 55 60
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
 65 70 75

[illegible]

					365					370				375
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				380					385					390
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				395					400					405
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				410					415					420
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Glu	Ala	Ser	Thr	Ala
				425					430					435
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val
				440					445					450
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala
				455					460					465
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ala	Gly	Ser	Gly	Thr	Ala
				470					475					480
Ala	Leu	Thr	Gly	Met	His	Thr	Thr	Ser	His	Ser	Ala	Ser	Thr	Ala
				485					490					495
Val	Ser	Glu	Ala	Lys	Pro	Gly	Gly	Ser	Leu	Val	Pro	Trp	Glu	Ile
				500					505					510
Phe	Leu	Ile	Thr	Leu	Val	Ser	Val	Val	Ala	Ala	Val	Gly	Leu	Phe
				515					520					525
Ala	Gly	Leu	Phe	Phe	Cys	Val	Arg	Asn	Ser	Leu	Ser	Leu	Arg	Asn
				530					535					540
Thr	Phe	Asn	Thr	Ala	Val	Tyr	His	Pro	His	Gly	Leu	Asn	His	Gly
				545					550					555
Leu	Gly	Pro	Gly	Pro	Gly	Gly	Asn	His	Gly	Ala	Pro	His	Arg	Pro
				560					565					570
Arg	Trp	Ser	Pro	Asn	Trp	Phe	Trp	Arg	Arg	Pro	Val	Ser	Ser	Ile
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Ala	Met	Glu	Met	Ser	Gly	Arg	Asn	Ser	Gly	Pro				
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<210> 244
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 244
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gaagcaccag cctttatctc ttcacc 26

<210> 245
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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic sequence.

<400> 245
 gtcagagttg gtggctgtgc tagc 24

<210> 246
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 246
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<210> 247
 <211> 957
 <212> DNA
 <213> Homo sapiens

<400> 247
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 cccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200
 agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250
 gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300
 ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350
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 gaagcagaga agcttggcca tggggtcaac aacgctgctg gacaggcccg 450
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 ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 550
 caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240

Ser Val Ala Asn Ile Met Pro
245

<210> 249
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 249
caatatgcat cttgcacgtc tgg 23

<210> 250
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 250
aagcttctct gcttcctttc ctgc 24

<210> 251
<211> 43
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-43
<223> Synthetic construct.

<400> 251
tgacccatt gagaagggtca ttgaagggat caaccgaggg ctg 43

<210> 252
<211> 3781
<212> DNA
<213> Homo sapiens

<400> 252

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ggggcggaac gcggggcgga gctgccgccc gtgagtccgg ccgagccacc 200
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 gtctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253
 <211> 837
 <212> PRT
 <213> Homo sapiens

<400> 253
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 Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser
 35 40 45
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
 50 55 60
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
 65 70 75
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80					85					90				
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile
				125					130					135
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly
				140					145					150
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn
				155					160					165
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp
				170					175					180
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala
				185					190					195
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe
				200					205					210
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro
				215					220					225
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe
				230					235					240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly
				245					250					255
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu
				260					265					270
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile
				275					280					285
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp
				290					295					300
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp
				305					310					315
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro
				320					325					330
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr
				335					340					345
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val
				350					355					360
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys
				365					370					375

Glu Val Asn Arg	Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro	380	385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg	395	400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys	Asp His Phe Leu Met Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val	Pro Gly Leu His His Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His	Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser	His Ser Gly Val Val Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser	Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val			

665					670					675				
Glu	Asp	Gly	Val	Ala	Asp	Gln	Thr	Asp	Glu	Gly	Gly	Ser	Val	Pro
				680					685					690
Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys
				695					700					705
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val
				710					715					720
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe
				725					730					735
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln
				740					745					750
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu
				755					760					765
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr
				770					775					780
Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro
				785					790					795
Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile
				800					805					810
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg
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Val	Arg	Leu	Gly	Ser	Glu	Ile	Arg	Asp	Ser	Val	Val			
				830					835					

<210> 254
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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 254
 agcccgtagca gaatctgctc ctgg 24

<210> 255
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 255
tgaagccagg gcagcgtoct ctgg 24

<210> 256
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 256
gtacaggctg cagttggc 18

<210> 257
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 257
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 258
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
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agggcgggac gggagcccg actcgtctgc cgccgccgctc gtcgccgtcg 150

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cgcccagacc	gccgctagcg	gcgcgccggg	atggtcccct	cttaaaggcg	250
caggccgcgg	cggcgggggg	gggtgtgcgg	aacaaagcgc	cggcgcgggg	300
cctgcggggcg	gctcgggggg	gcgcgatggg	gcggcggggc	cgcggcggcg	350
gcggcgctgc	ccgggcccgg	cctcgcgggc	ctagggcggg	ctggccctccg	400
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gcttcccagg	ccggcggggg	gcgcggcgat	gcgcgcgggg	cgcagctctg	700
gccgcccggc	tccgacccag	atggcgggcc	gcgcgacagg	aactttctct	750
tcgtagggagt	catgaccgcc	cagaaatacc	tgcagactcg	ggccgtggcc	800
gcctacagaa	catgggtccaa	gacaattcct	gggaaagttc	agttctttctc	850
aagtgaggg	tctgacacat	ctgtaccaat	tccagtagtg	ccactacggg	900
gtgtggacga	ctcctacccg	cccagaaga	agtccttcat	gatgctcaag	950
tacatgcacg	accactactt	ggacaagtat	gaatggttta	tgagagcaga	1000
tgatgacgtg	tacatcaaag	gagaccgtct	ggagaacttc	ctgaggagtt	1050
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acattagaga	tctccataac	agtaaaattc	accaagctat	cacattacac	1400
cccaacaaaa	accacccta	ccagtacagg	ctccacagct	acatgctgag	1450
ccgcaagata	tccgagctcc	gccatgcac	aatacagctg	caccgcgaaa	1500
ttgtcctgat	gagcaaatac	agcaacacag	aaattcataa	agaggacctc	1550
cagctgggaa	tccctccctc	cttcatgagg	tttcagcccc	gccagcgaga	1600

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 ggggtgaacc catgtatggg gctgagtaca tcctggacct gctgcttctg 1850
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 tttcaattct gactccaacc ctgacaaggc caaacaagtt gaactgatga 2250
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 ccagtgaaca atatttttct attgtacttt tcgaaccatt ttgtctcatt 4500

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aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

Met Ala Ala Arg Gly Arg Arg Ala Trp Leu Ser Val Leu Leu Gly
1 5 10 15

Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530					535					540				
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu
				545					550					555
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu
				560					565					570
Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu
				575					580					585
Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln
				590					595					600
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu
				605					610					615
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys
				620					625					630
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg
				635					640					645
Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe
				650					655					660
Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser
				665					670					675
Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn
				680					685					690
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg
				695					700					705
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp
				710					715					720
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe
				725					730					735
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe
				740					745					750
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly
				755					760					765
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met
				770					775					780
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn
				785					790					795
Asn	Gly	Ser	Val	Arg	Thr	Ala								
				800										

<210> 261
 <211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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tgacaccttc ctttctggcc ttgaggttcc cagcctggtg gcccaggac 100
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccctattc 500
 tggtcgatca aaccaaaaaa tgtttccatt gttttgcatg cagaggaacc 550
 ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600
 aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650
 ccatatgtta cctcatataa gtcacctgtc accactttag ataagagcac 700
 tggcattgag atctctacag aatcagaaga tgttcctcag ctctcagggtg 750
 aaactgcatg agaaaaaacc gaagagtttg gaaagcacc agagagtttg 800
 aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtgc 850
 acaggcactt cttagtgcac ccagcaaccc agcatataga gaagatattg 900
 aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950
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 aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050
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<210> 265
 <211> 350
 <212> PRT
 <213> Homo sapiens

<400> 265
 Met Lys Pro Leu Val Leu Leu Val Ala Leu Leu Leu Trp Pro Ser
 1 5 10 15
 Ser Val Pro Ala Tyr Pro Ser Ile Thr Val Thr Pro Asp Glu Glu
 20 25 30
 Gln Asn Leu Asn His Tyr Ile Gln Val Leu Glu Asn Leu Val Arg
 35 40 45
 Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser

50					55					60				
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
				80					85					90
Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly
				95					100					105
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro
				110					115					120
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala
				125					130					135
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu
				140					145					150
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val
				155					160					165
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro
				170					175					180
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu
				185					190					195
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys
				200					205					210
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp
				215					220					225
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala
				230					235					240
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu
				245					250					255
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala
				260					265					270
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro
				275					280					285
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile
				290					295					300
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp
				305					310					315
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val
				320					325					330
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala
				335					340					345

ccaacaatgg gtattgggtc ctcagactga caacagaaca tttgtatttc 1300
acattcaatc cccattttat cagcctcccc cccagcacc ctcctacacg 1350
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caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt 2300
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gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400

aaa 2403

<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

20										25					30				
Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu					
				35					40					45					
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe					
				50					55					60					
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser					
				65					70					75					
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp					
				80					85					90					
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr					
				95					100					105					
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile					
				110					115					120					
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly					
				125					130					135					
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile					
				140					145					150					
Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala					
				155					160					165					
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg					
				170					175					180					
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile					
				185					190					195					
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu					
				200					205					210					
Ala	Glu	Gln	Ser	His	Glu	Val	Glu	Ser	Lys	Val	Leu	Ile	Gly	Glu					
				215					220					225					
Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu					
				230					235					240					
Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile					
				245					250					255					
Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp					
				260					265					270					
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys					
				275					280					285					
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys					
				290					295					300					
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro					
				305					310					315					

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val
320 325 330

Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val
335 340 345

Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp
350 355 360

Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn
365 370 375

Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr
380 385 390

Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr
395 400 405

Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe
410 415 420

Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys
425 430 435

Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr
440 445 450

Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp
455 460 465

Gly

<210> 268
<211> 2103
<212> DNA
<213> Homo sapiens

<400> 268
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gtcatcttca tatccctgat tgccttggca gtgtgcattg gactcactgt 150
tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaaatgc 300
attttataaaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350
agttcagtcacacagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
agatttcact ctactgagga tcttgaaact gtagataaaa ttgttcaact 450
tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
 ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
 caggatcggt ggtgggacag aagtagaaga ggggtgaatgg ccctggcagg 650
 ctagcctgca gtgggatggg agtcatcgct gtggagcaac cttaattaat 700
 gccacatggc ttgtgagtgc tgctcactgt tttaacaacat ataagaaccc 750
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 aacgggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850
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 tatgtgctgg ctcccttagaa ggaaaaacag atgcatgcca gggtgactct 1150
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 aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctggtgttt 1250
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 taagagacaa aagcctcatg gaacagataa catttttttt tgttttttgg 1350
 gtgtggaggc cattttttaga gatacagaat tggagaagac ttgcaaaaca 1400
 gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc 1450
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 tgtcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata 1550
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 cagaattttg acttgttgac ataaatttgt aatgcatata tacaatttga 1650
 agcaactcct ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700
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 tcccctacat ttatttgga cagaaaagta ttaggtgttt ttcttagtgg 1800
 aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850
 aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900
 tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050
 ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100
 cca 2103

<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269
 Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys
 1 5 10 15
 Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
 20 25 30
 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro
230 235 240

Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys
245 250 255

Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
260 265 270

His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser
275 280 285

Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp
290 295 300

Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly
305 310 315

Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg
320 325 330

Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro
335 340 345

Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly
350 355 360

Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly
365 370 375

Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly
380 385 390

Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly
395 400 405

Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys
410 415 420

Thr Gly Ile

<210> 270
<211> 1170
<212> DNA
<213> Homo sapiens

<400> 270
gtcgaagggtt ataaaagctt ccagccaaac ggcattgaag ttgaagatac 50
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cagacgtcag ctggtggatt cccgctgcat caaggcctac ccaactgtctc 150
catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200
ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

gatgagactg agacggcgtg gccgcctttg ccggctgtcc cctgcgacta 300
 cgaccactgc cgacacctgc aggtgccctg caaggagcta cagaggggtcg 350
 ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400
 gacccgccgc gcatgggaga agtgcgcatt gcggccgaag agggccgcgc 450
 agtggccac tgggtgtgcc ccttctcccc ggctctccac tactggctgc 500
 tgctttggga cggcagcgag gctgcgcaga aggggcccc gctgaacgct 550
 acggtccgca gagccgaact gaaggggctg aagccagggg gcatttatgt 600
 cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650
 ctggaggaga gggcctcgag ggggccgaca tccctgcctt cgggccttgc 700
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 acttctgcct gcgcgatcgc tggggctgcc cgcgccgagc cgcgcgccga 850
 gccgcagggg cgctctgaaa ggggcctggg ggcattctcg gcacagacag 900
 cccacactgg ggcgtcagc ctggcccccg ggaaagagga aaaccgctg 950
 cctccaggga gggctggacg gcgagctggg agccagcccc aggctccagg 1000
 gccacggcgg agtcatgggt ctcaggactg agcgcttggt taggtccggt 1050
 acttggcgct ttgtttcctg gctgaggtct gggaaggaat agaaaggggc 1100
 ccccaatttt tttttaagcg gccagataat aaataatgta acctttgcgg 1150
 ttaaaaaaaaa aaaaaaaaaa 1170

<210> 271
 <211> 238
 <212> PRT
 <213> Homo sapiens

<400> 271
 Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe
 1 5 10 15
 Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu
 20 25 30
 Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
 35 40 45
 Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
 50 55 60
 Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
 65 70 75

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
80 85 90

Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys
95 100 105

Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
110 115 120

Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
125 130 135

Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
140 145 150

Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
155 160 165

Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
170 175 180

Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
185 190 195

Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
200 205 210

Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
215 220 225

Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
230 235

<210> 272
<211> 2397
<212> DNA
<213> Homo sapiens

<400> 272
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cccaggcggg cgtggggcac cgggccccagc gccgacgatc gctgccgttt 150
tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250
acgccctcaa tctgctcttt tggttaatgt ccatcagtgt gttggcagtt 300
tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350
aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcac 400
cggatcatgat tgctgtttgc tgtttcctta tcattgtggg gatggttagga 450
tattgtggaa cggtgaaaag aaatctgttg cttcttgcac ggtactttgg 500

aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttggacat 550
atgaacagga acttatgggt ccagtacaat ggtcagatat ggtcactttg 600
aaagccagga tgacaaatta tggattacct agatatcggt ggcttactca 650
tgcttggaaat ttttttcaga gagagttaa gtgctgtgga gtagtatatt 700
tactgactg gttggaaatg acagagatgg actggcccc agattcctgc 750
tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800
cagtgcctt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850
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gtattatgat agaagggagc ctgggacaga ccaaatgatg tccttgaaga 1000
atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca 1050
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caacttggtt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350
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actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900
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agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa 2000
 cttagttgat tcagaaagga cttgtatgct gtttttctcc caaatgaaga 2050
 ctctttttga cactaaacac tttttaaaaa gcttatcttt gccttctcca 2100
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 ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200
 tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta 2250
 cacagattat taaatTTTTT tacaagagta tagtatattt atttgaaatg 2300
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 atggaaagaa aattaaaatg tgtcaataaa tattttctag agagtaa 2397

<210> 273
 <211> 305
 <212> PRT
 <213> Homo sapiens

<400> 273
 Met Ala Arg Glu Asp Ser Val Lys Cys Leu Arg Cys Leu Leu Tyr
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 Ala Leu Asn Leu Leu Phe Trp Leu Met Ser Ile Ser Val Leu Ala
 20 25 30
 Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
 35 40 45
 Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
 50 55 60
 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
 65 70 75
 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
 80 85 90
 Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
 95 100 105
 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
 110 115 120
 Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
 125 130 135
 Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
 140 145 150
 Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
 155 160 165
 Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

	170		175		180
Cys Cys Val Arg	Glu Phe Pro Gly Cys	Ser Lys Gln Ala His	Gln		
	185		190		195
Glu Asp Leu Ser	Asp Leu Tyr Gln Glu	Gly Cys Gly Lys Lys	Met		
	200		205		210
Tyr Ser Phe Leu	Arg Gly Thr Lys Gln	Leu Gln Val Leu Arg	Phe		
	215		220		225
Leu Gly Ile Ser	Ile Gly Val Thr Gln	Ile Leu Ala Met Ile	Leu		
	230		235		240
Thr Ile Thr Leu	Leu Trp Ala Leu Tyr	Tyr Asp Arg Arg Glu	Pro		
	245		250		255
Gly Thr Asp Gln	Met Met Ser Leu Lys	Asn Asp Asn Ser Gln	His		
	260		265		270
Leu Ser Cys Pro	Ser Val Glu Leu Leu	Lys Pro Ser Leu Ser	Arg		
	275		280		285
Ile Phe Glu His	Thr Ser Met Ala Asn	Ser Phe Asn Thr His	Phe		
	290		295		300
Glu Met Glu Glu	Leu				
	305				

<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

<400> 274
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 ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgtctgc 150
 cttgggggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200
 agagccagca tgttacagga tctgacagt gatcaacctc tgaacagcct 250
 cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa 300
 aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350
 attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg 400
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aaacagccag gagcttcgca tgcggaactc aagtggggccc tgtctctcag 750
gctccctggt ctccctgcac tgtcttgccct gtgggaagag cctgaagacc 800
ccccgtgtgg tgggtgggga ggaggcctct gtggattctt ggccttggca 850
ggtcagcatc cagtaagaca aacagcacgt ctgtggaggg agcatcctgg 900
acccccactg ggctcctcac gcagccact gcttcaggaa acataccgat 950
gtgttcaact ggaaggtgag ggcaggctca gacaaactgg gcagcttccc 1000
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tccagccacc cactctgga tcattggatg gggctttacg aagcagaatg 1200
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tcaactgtggg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900
tcttcacca tcccaagcc tactagagca agaaaccagt tgtaatatata 1950
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[illegible]

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp
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Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg
20 25 30

Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys
				260					265					270
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp
				275					280					285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr
				290					295					300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro
				305					310					315
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn
				320					325					330
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val
				335					340					345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu
				350					355					360
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val
				365					370					375
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser
				380					385					390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys
				395					400					405
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr
				410					415					420
Leu	Asn	Trp	Ile	Tyr	Asn	Val	Trp	Lys	Ala	Glu	Leu			
				425					430					

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276
 gggctgagggc actgagagac cgaaagcct ggcattccag agggagggaa 50
 acgcagcggc atccccaggc tccagagctc cctggtgaca gtctgtggct 100
 gagcatggcc ctccagccc tgggcctgga ccctggagc ctccctgggcc 150
 ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
 ggaggcgggc agggggccat gccaggggc agatactatg caggggatga 250
 acgtagggca cttagcttct tccaccagaa gggcctccag gattttgaca 300
 ctctgctcct gagtggatgat ggaaatactc tctacgtggg ggctcgagaa 350
 gccattctgg ccttgatata ccaggatcca ggggtcccca ggctaaagaa 400

catgataccg tggccagcca gtgacagaaa aaagagtga tgtgccttta 450
 agaagaagag caatgagaca cagtgtttca acttcatccg tgtcctgggt 500
 tcttacaatg tcacccatct ctacacctgc ggcaccttcg ccttcagccc 550
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 aagcatacgg ctgtcttggt ggatgggatg ctctattctg gtactatgaa 700
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<213> Homo sapiens
<400> 277

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50 55 60
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Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln
80 85 90
Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala
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Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn
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Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn
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140 145 150
Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser
155 160 165
Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro
170 175 180
Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser
185 190 195
Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg
200 205 210
Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg
215 220 225
Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
230 235 240
Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp
245 250 255
Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys
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Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr
275 280 285
Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro

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Thr	Ser	Arg	Trp	Thr 365	Thr	Tyr	Arg	Gly	Pro 370	Glu	Thr	Asn	Pro	Arg 375
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Pro	Leu	Leu	Val	Lys 410	Ser	Gly	Val	Glu	Tyr 415	Thr	Arg	Leu	Ala	Val 420
Glu	Thr	Ala	Gln	Gly 425	Leu	Asp	Gly	His	Ser 430	His	Leu	Val	Met	Tyr 435
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Asp	Ser	Ser	Ala	His 455	Leu	Val	Glu	Glu	Ile 460	Gln	Leu	Phe	Pro	Asp 465
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Gly	Asn	Pro	Glu	Trp 545	Ala	Cys	Ala	Ser	Gly 550	Pro	Met	Ser	Arg	Ser 555
Leu	Arg	Pro	Gln	Ser 560	Arg	Pro	Gln	Ile	Ile 565	Lys	Glu	Val	Leu	Ala 570
Val	Pro	Asn	Ser	Ile 575	Leu	Glu	Leu	Pro	Cys 580	Pro	His	Leu	Ser	Ala 585

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
590 595 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
605 610 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
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Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
635 640 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
650 655 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 670 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 685 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 700 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 715 720

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<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

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Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile	35	40	45	
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg	50	55	60	
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln	65	70	75	
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys	80	85	90	
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly	95	100	105	
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln	110	115	120	
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys	125	130	135	
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys	140	145	150	
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile	155	160	165	
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro	170	175	180	
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met	185	190	195	
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe	200	205	210	
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile	215	220	225	
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu	230	235	240	
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe	245	250	255	
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Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys
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Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn
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Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His
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Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile
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Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu
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Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys
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Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu
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Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser
				425					430					435
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser
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Pro	Thr	Gln	Arg	Leu	Val	Gly	Trp	Ile	Asp	His	Val	Leu	Gln	Thr
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Gly	Gly	Ala	Thr	His	Leu	Lys	Pro	Tyr	Val	Phe	Gln	Gln	Pro	Trp
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His	Glu	Gln	Tyr	Leu	Phe	Asp	Val	Phe	Val	Phe	Leu	Leu	Gly	Leu
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Thr	Leu	Gly	Thr	Leu	Trp	Leu	Cys	Gly	Lys	Leu	Leu	Gly	Met	Ala
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 <212> DNA
 <213> Artificial

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<211> 205
<212> PRT
<213> Homo sapiens
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Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys	
				35					40					45	
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly	
				50					55					60	
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala	
				65					70					75	
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	
				80					85					90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	
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Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	
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Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	
				125					130					135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	
				140					145					150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	
				155					160					165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser	

170	175	180
Leu Arg Leu Arg Arg Gly Asn Leu Leu	Gly Gly Trp Lys Tyr Ser	
185	190	195

Ser Phe Ser Gly Phe Leu Ile Phe Pro	Leu
200	205

<210> 288
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 288
 aggcagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 289
 cagagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 290
 ctgtgtact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 291
 gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50
 tagccgcccc gcctcgacgc cgtcccggga cccctgtgct ctgcgcgaag 100
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200
 ccgcctactc cggggtcctg cgcggcgagc gtcaggccga ggctgaccgg 250
 agccagcgct ctacacggagg acctgcgctg tcgcgcgagg ggtctgggag 300
 atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350
 tcacctggct caataggtcc aaggtggaaa agcagctaca ggtcatctca 400
 gtgctccagt gggtcctgtc cttccttgta ctgggagtgg cctgcagtgc 450
 catcctcatg tacatattct gactgattg ctggctcatc gctgtgctct 500
 acttcacttg gctgggtgtt gactggaaca caccaagaa aggtggcagg 550
 aggtcacagt gggtcgaaa ctgggctgtg tggcgctact ttcgagacta 600
 ctttcccatc cagctggtga agacacacaa cctgctgacc accaggaact 650
 atatcttttg ataccacccc catggatatca tgggcctggg tgccttctgc 700
 aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750
 gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800
 agtacctgat gtctggagggt atctgccctg tcagccggga caccatagac 850
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 agagcccatc accatcccca agctggagca cccaaccag caagacatcg 1250
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 ttgctctgt aaatttgaa gtgtcatggg tgtctgtggg ttatttataa 1450
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550
 aaaaaaaaaa aaaaaaaaaa 1570

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<210> 292
<211> 388
<212> PRT
<213> Homo sapiens
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<400> 292

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Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val Tyr	
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp	Gly Arg Trp Val Gln	
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe His	
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro Tyr	
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly	Glu Pro Ile Thr Ile Pro	
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His Thr	
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu	Phe Asp Lys His Lys Thr	
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val	Leu Glu Val Asn	
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 295
 aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
 <211> 3060
 <212> DNA
 <213> Homo sapiens

<400> 296
 gggcgggcgg atggggggccg gggggcggcg ggcgcgcact cgctgaggcc 50
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 cggggcccg cgaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
 gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
 ggctctgctg accttgtgcc ttggacggct gtcctcagcg agggggccgtg 250
 caccgcgtcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300
 gtctgtgctg cactgtctgg tcggctttgt ctctgtgtg agtggctctg 350
 tcatcaactt cgtccagctg tgcacgctgg cgtcttgccc ggtcagcaag 400
 cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450
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 cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950
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 ctctacggga agaagtacga ggcggacatg tgcgtgagga gatttctct 1050
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 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccacacta 2950
 ccagggagac tgaagtggga ggatcgcttg ggcatgagaa gtcgaggctg 3000
 cagtgaagtc aggttgtgct actgcattcc agcctggaca acagagttag 3050
 accctgtctc 3060

<210> 297
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 297
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
 1 5 10 15
 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
 20 25 30
 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
 35 40 45
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
 50 55 60
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
 65 70 75
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala
 80 85 90
 Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly
 95 100 105
 Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val
 110 115 120
 Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
 125 130 135
 Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
 140 145 150
 Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
 155 160 165

Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe
170 175 180

Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys
185 190 195

Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly
200 205 210

Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val
215 220 225

Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
230 235 240

Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val
245 250 255

Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala
260 265 270

Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln
275 280 285

Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys
290 295 300

Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala
305 310 315

Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe
320 325 330

Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val
335 340 345

Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Glu Ser Leu
350 355 360

Glu Pro Gly Arg Trp Arg Leu Gln
365

<210> 298
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 298
cttcctctgt ggggtggacca tgtg 24

<210> 299
<211> 21
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggctcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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 tcagtttgtc ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200
 cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250
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 tcttttgctg gacactgttc cctgcccccc ccatactctt cctacttaat 550
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 gtcccagcta cttgggaggg tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggagggtt cagtgaagcg agatcaggcc actgtattcc aaccagggtg 1300
 acagagttag actctatgtc caaaaaaaaa aaaa 1334

<210> 302
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 302
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 His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe
 20 25 30
 Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly
 35 40 45
 Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val
 50 55 60
 Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp
 65 70 75
 Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr
 80 85 90
 Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln
 95 100 105
 Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu
 110 115 120
 Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr
 125 130 135
 Cys Gly Val Leu Leu Ser Phe Leu

140

<210> 303
<211> 1768
<212> DNA
<213> Homo sapiens

<400> 303
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tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
tatgctgtgg tggctagtgc tctactcct acctacatta aaatctgttt 200
tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
ttctaccac accgtccct cgaagccggg gacagcctca ccttgctggc 350
ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400
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tgggccttgc cctggccgta gaagggattg acaagccga agatttcata 500
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 ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccagggtgcat 1450
 taagaatcag ttattgccgg gtgtgggtggc ctgtaatgcc aacattttgg 1500
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550
 gccaacatgg tgaaaccctt gtctctacta aaaatacaaa aaaactagcc 1600
 aggcattgtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
 ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750
 aattatgggt atttgtaa 1768

<210> 304
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 304
 Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser
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 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
 20 25 30
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
 65 70 75
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
 80 85 90
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
 95 100 105
 Arg Arg Arg Asp

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305

gcggggcccg	gagtccgaga	cctgtcccag	gagctccagc	tcacgtgacc	50
tgtcactgcc	tcccgccgcc	tcctgcccgc	gccatgaccc	agccggtgcc	100
cgggctctcc	gtgcccgcg	cgctggccct	gggctcagcc	gcactgggcg	150
ccgccttcgc	cactggcctc	ttcctgggga	ggcggtgccc	cccatggcga	200
ggccggcgag	agcagtgcct	gcttcccccc	gaggacagcc	gcctgtggca	250
gtatcttctg	agccgctcca	tgcgggagca	ccgggcgctg	cgaagcctga	300
ggctgctgac	cctggagcag	ccgcaggggg	attctatgat	gacctgcgag	350
caggcccagc	tcttgccaa	cctgggcgcg	ctcatccagg	ccaagaaggc	400
gctggacctg	ggcaccttca	cgggctactc	cgccctggcc	ctggccctgg	450
cgctgcccgc	ggacggggcg	gtggtgacct	gcgaggtgga	cgcgcagccc	500
ccggagctgg	gacggccctt	gtggaggcag	gccgaggcgg	agcacaagat	550
cgacctccgg	ctgaagcccg	ccttgagagc	cctggacgag	ctgctggcgg	600
cgggcgaggc	cggcaccttc	gacgtggccg	tggtggatgc	ggacaaggag	650
aactgctccg	cctactacga	gcgctgcctg	cagctgctgc	gacccggagg	700
catcctcgcc	gtcctcagag	tcctgtggcg	cgggaagggtg	ctgcaacctc	750
cgaaagggga	cgtaggcggcc	gagtgtgtgc	gaaacctaaa	cgaacgcata	800
cggcgggacg	tcagggtcta	catcagcctc	ctgcccctgg	gcgatggact	850
caccttggcc	ttcaagatct	agggctggcc	cctagtgagt	gggctcgagg	900
gagggttgcc	tgggaacccc	aggaattgac	cctgagtttt	aaattcgaaa	950
ataaagtggg	gctgggacac	aaaaaaaaaa	aaaaaaaaaa	989	

```
<210> 306
<211> 262
<212> PRT
<213> Homo sapiens
```

```

<400> 306
Met Thr Gln Pro Val Pro Arg Leu Ser Val Pro Ala Ala Leu Ala
  1          5          10          15

Leu Gly Ser Ala Ala Leu Gly Ala Ala Phe Ala Thr Gly Leu Phe
          20          25          30

Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys
          35          40          45

Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser
          50          55          60

```

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
65 70 75

Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
80 85 90

Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
95 100 105

Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
110 115 120

Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
125 130 135

Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
140 145 150

Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
155 160 165

Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
170 175 180

Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
185 190 195

Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
200 205 210

Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
215 220 225

Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
230 235 240

Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
245 250 255

Leu Thr Leu Ala Phe Lys Ile
260

<210> 307
<211> 2272
<212> DNA
<213> Homo sapiens

<400> 307
ccgccgccgc agccgctacc gccgctgcag ccgctttccg cggcctgggc 50
ctctcgccgt cagcatgccca cacgccttca agcccgggga cttggtgttc 100
gctaagatga agggctaccc tcaactggcct gccaggatcg acgacatcg 150
ggatggcgcc gtgaagcccc cacccaacaa gtaccccatc tttttctttg 200
gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300
 agggctgtgg gagatccaga acaacccccca cgccagctac agcgcccctc 350
 cgccagtggg ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400
 ggcagtggcg ctgacgagga cgatgaggac cgggggggtca tggccgtcac 450
 agcggtaacc gccacagctg ccagcgacag gatggagagc gactcagact 500
 cagacaagag tagcgacaac agtggcctga agaggaagac gcctgcgcta 550
 aagatgtcgg tctcgaaacg agcccgaaag gcctccagcg acctggatca 600
 ggccagcgtg tccccatccg aagaggagaa ctcgaaagc tcatctgagt 650
 cggagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggtc 700
 cgggcgccac ggagggggccc tctgggggga cggaaaaaaa agaaggcgcc 750
 gtcagcctcc gactccgact ccaaggccga ttcggacggg gccaagcctg 800
 agccggtggc catggcgcgg tcggcgctct cctcctctc ttcctcctcc 850
 tctccgact ccgatgtgtc tgtgaagaag cctccgaggg gcaggaagcc 900
 agcggagaag cctctccga agccgcgagg gcggaaaccg aagcctgaac 950
 ggctccgtc cagctccagc agtgacagtg acagcgacga ggtggaccgc 1000
 atcagtgagt ggaagcggcg ggacgaggcg cggaggcgcg agctggaggc 1050
 ccggcgggcg cgagagcagg aggaggagct gcggcgctg cgggagcagg 1100
 agaaggagga gaaggagcgg aggcgcgagc gggccgaccg cggggagggt 1150
 gagcggggca gcggcggcag cagcggggac gagctcaggg aggacgatga 1200
 gcccgtaag aagcggggac gcaagggccg gggccggggt ccccgctcct 1250
 cctctgactc cgagcccag gccgagctgg agagagaggc caagaaatca 1300
 gcgaagaagc cgcagtcctc aagcacagag cccgccagga aacctggcca 1350
 gaaggagaag agagtgcggc ccgaggagaa gcaacaagcc aagcccgtga 1400
 aggtggagcg gacccggaag cgggccgagg gcttctcgat ggacaggaag 1450
 gtagagaaga agaaagagcc ctccgtggag gagaagctgc agaagctgca 1500
 cagtgagatc aagtttgccc taaaggtcga cagcccggac gtgaagaggt 1550
 gcctgaatgc ctagaggag ctgggaaccc tgcaggtgac ctctcagatc 1600
 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttcgccgtta 1650
 caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tatacccggc 1700

tcaagtcgcg ggtcctcggc ccaaagatcg aggcggtgca gaaagtgaac 1750
aaggctggga tggagaagga gaaggccgag gagaagctgg ccggggagga 1800
gctggccggg gaggaggccc cccaggagaa ggcggaggac aagcccagca 1850
ccgatctctc agccccagtg aatggcgagg ccacatcaca gaagggggag 1900
agcgcagagg acaaggagca cgaggagggt cgggactcgg aggagggggc 1950
aaggtgtggc tcctctgaag acctgcacga cagcgtacgg gaggggtccc 2000
acctggacag gcctgggagc gaccggcagg agcgcgagag ggcacggggg 2050
gactcggagg ccctggacga ggagagctga gccgcgggca gccaggccca 2100
gccccgcgcc gagctcaggc tgcccctctc cttccccggc tcgcaggaga 2150
gcagagcaga gaactgtggg gaacgctgtg ctgtttgtat ttgttccctt 2200
gggttttttt ttctgcta atttctgtga tttccaacca acatgaaatg 2250
actataaacg gttttttaat ga 2272

<210> 308
<211> 671
<212> PRT
<213> Homo sapiens

<400> 308
Met Pro His Ala Phe Lys Pro Gly Asp Leu Val Phe Ala Lys Met
1 5 10 15
Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Asp Ile Ala Asp
20 25 30
Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe
35 40 45
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
50 55 60
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
65 70 75
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
80 85 90
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
95 100 105
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
110 115 120
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
125 130 135
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser

	140	145	150
Asp Asn Ser Gly	Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met	Ser
	155	160	165
Val Ser Lys Arg	Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln	Ala
	170	175	180
Ser Val Ser Pro	Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser	Glu
	185	190	195
Ser Glu Lys Thr	Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys	Ala
	200	205	210
Ala Val Arg Ala	Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys	Lys
	215	220	225
Lys Lys Ala Pro	Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp	Ser
	230	235	240
Asp Gly Ala Lys	Pro Glu Pro Val Ala	Met Ala Arg Ser Ala	Ser
	245	250	255
Ser Ser Ser Ser	Ser Ser Ser Ser Ser	Asp Ser Asp Val Ser	Val
	260	265	270
Lys Lys Pro Pro	Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu	Pro
	275	280	285
Lys Pro Arg Gly	Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser	Ser
	290	295	300
Ser Ser Ser Asp	Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser	Glu
	305	310	315
Trp Lys Arg Arg	Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala	Arg
	320	325	330
Arg Arg Arg Glu	Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu	Gln
	335	340	345
Glu Lys Glu Glu	Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg	Gly
	350	355	360
Glu Ala Glu Arg	Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu	Arg
	365	370	375
Glu Asp Asp Glu	Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg	Gly
	380	385	390
Arg Gly Pro Pro	Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu	Leu
	395	400	405
Glu Arg Glu Ala	Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser	Ser
	410	415	420
Thr Glu Pro Ala	Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val	Arg
	425	430	435

```

Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
    440                                445                                450
Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
    455                                460                                465
Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
    470                                475                                480
Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
    485                                490                                495
Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
    500                                505                                510
Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
    515                                520                                525
Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
    530                                535                                540
Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
    545                                550                                555
Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys
    560                                565                                570
Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala
    575                                580                                585
Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala
    590                                595                                600
Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
    605                                610                                615
Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
    620                                625                                630
Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
    635                                640                                645
Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala
    650                                655                                660
Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser
    665                                670

```

<210> 309
 <211> 3871
 <212> DNA
 <213> Homo sapiens

<400> 309
 gttggttctc ctggatcttc accttaccaa ctgcagatct tgggactcat 50
 cagcctcaat aattatatta aattaacacc atttgaaaga gaacattgtt 100

tttcaaagga aaagtggaat atggaagagg tagtgctgga ggagttgcag 1600
 atattcaagc actcatcaat catcttgaac atggaattgt ctctgaagca 1650
 gcaacaattg tacattgggt cccgagatgg attagttcag ctctccttgc 1700
 acagatgcga cacttatggg aaagcttgcg cagactgttg tcttgccaga 1750
 gacccctact gtgcctggga tggaaatgca tgctctcgat atgctcctac 1800
 ttctaaaagg agagctagac gccaaagatgt aaaatatggc gacccaatca 1850
 cccagtgtcg ggacatcgaa gacagcatta gtcatgaaac tgctgatgaa 1900
 aagggtgattt ttggcattga atttaactca acctttctgg aatgtatacc 1950
 taaatcccaa caagcaacta ttaaattgta tatccagagg tcaggggatg 2000
 agcatcgaga ggagttgaag cccgatgaaa gaatcatcaa aacggaatat 2050
 gggctactga ttcgaagttt gcagaagaag gattctggga tgtattactg 2100
 caaagcccag gagcacactt tcatccacac catagtgaag ctgactttga 2150
 atgtcattga gaatgaacag atggaaaata cccagagggc agagcatgag 2200
 gaggggcagg tcaaggatct attggctgag tcacggttga gatacaaaga 2250
 ctacatccaa atccttagca gcccaaactt cagcctcgac cagtactgcg 2300
 aacagatgtg gcacagggag aagcggagac agagaaacaa ggggggcca 2350
 aagtggaagc acatgcagga aatgaagaag aaacgaaatc gaagacatca 2400
 cagagacctg gatgagctcc ctagagctgt agccacgtag ttttctactt 2450
 aatttaaaga aaagaattcc ttacctataa aaacattgcc ttctgttttg 2500
 tatatccctt atagtaattc ataaatgctt cccatggagt tttgctaagg 2550
 cacaagacaa taatctgaat aagacaatat gtgatgaata taagaaaggg 2600
 caaaaaattc atttgaacca gttttccaag aacaaatctt gcacaagcaa 2650
 agtataagaa ttatcctaaa aatagggggg ttacagttgt aaatgtttta 2700
 tgttttgagt tttggaattt attgtcatgt aaatagttga gctaagcaag 2750
 ccccgaattt gatagtgtat aagggtgctt attccctcga atgtccatta 2800
 agcatggaat ttaccatgca gttgtgctat gttcttatga acagatatat 2850
 cattcctatt gagaaccagc taccttgtgg tagggaataa gaggtcagac 2900
 acaaattaag acaactccca ttatcaacag gaactttctc agtgagccat 2950
 tcactcctgg agaattggtat aggaatttgg agaggtgcat tatttctttc 3000

tggccactgg	ggttaaattt	agtgtactac	aacattgatt	tactgaaggg	3050
cactaatgtt	tccccagga	tttctattga	ctagtcagga	gtaacaggtt	3100
cacagagaga	agttggtgct	tagttatgtg	ttttttagag	tatatactaa	3150
gctctacagg	gacagaatgc	ttaataaata	ctttaataag	atatgggaaa	3200
atattttaat	aaaacaagga	aaacataatg	atgtataatg	catcctgatg	3250
ggaaggcatg	cagatgggat	ttgttagaag	acagaaggaa	agacagccat	3300
aaattctggc	tttggggaaa	actcatatcc	ccatgaaaag	gaagaacaat	3350
cacaaataaa	gtgagagtaa	tgtaatggag	ctcttttcac	tagggtataa	3400
gtagctgcca	atttgtaatt	catctgttaa	aaaaaatcta	gattataaca	3450
aactgctagc	aaaatctgag	gaaacataaa	ttcttctgaa	gaatcatagg	3500
aagagtagac	attttattta	taaccaatga	tatttcagta	tatatatttct	3550
ctcttttaaa	aaatatttat	catactctgt	atattatttc	tttttactgc	3600
ctttattctc	tcctgtatat	tggattttgt	gattatattt	gagtgaatag	3650
gagaaaacaa	tatataacac	acagagaatt	aagaaaatga	catttctggg	3700
gagtggggat	atatatttgt	tgaataacag	aacgagtgtg	aaattttaac	3750
aacggaaagg	gttaaattaa	ctctttgaca	tcttcactca	accttttctc	3800
attgctgagt	taatctgttg	taattgtagt	attgtttttg	taattttaaca	3850
ataaataagc	ctgctacatg	t			3871

```
<210> 310
<211> 777
<212> PRT
<213> Homo sapiens
```

```

<400> 310
Met Asn Ala Asn Lys Asp Glu Arg Leu Lys Ala Arg Ser Gln Asp
 1          5      10
Phe His Leu Phe Pro Ala Leu Met Met Leu Ser Met Thr Met Leu
      20      25      30
Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu
      35      40      45
Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
      50      55      60
Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
      65      70      75
Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

```

80									85					90	
Phe	Leu	Leu	Ser	Leu 95	Val	Asp	Leu	Asn	Lys 100	Asn	Phe	Lys	Lys	Ile 105	
Tyr	Trp	Pro	Ala	Ala 110	Lys	Glu	Arg	Val	Glu 115	Leu	Cys	Lys	Leu	Ala 120	
Gly	Lys	Asp	Ala	Asn 125	Thr	Glu	Cys	Ala	Asn 130	Phe	Ile	Arg	Val	Leu 135	
Gln	Pro	Tyr	Asn	Lys 140	Thr	His	Ile	Tyr	Val 145	Cys	Gly	Thr	Gly	Ala 150	
Phe	His	Pro	Ile	Cys 155	Gly	Tyr	Ile	Asp	Leu 160	Gly	Val	Tyr	Lys	Glu 165	
Asp	Ile	Ile	Phe	Lys 170	Leu	Asp	Thr	His	Asn 175	Leu	Glu	Ser	Gly	Arg 180	
Leu	Lys	Cys	Pro	Phe 185	Asp	Pro	Gln	Gln	Pro 190	Phe	Ala	Ser	Val	Met 195	
Thr	Asp	Glu	Tyr	Leu 200	Tyr	Ser	Gly	Thr	Ala 205	Ser	Asp	Phe	Leu	Gly 210	
Lys	Asp	Thr	Ala	Phe 215	Thr	Arg	Ser	Leu	Gly 220	Pro	Thr	His	Asp	His 225	
His	Tyr	Ile	Arg	Thr 230	Asp	Ile	Ser	Glu	His 235	Tyr	Trp	Leu	Asn	Gly 240	
Ala	Lys	Phe	Ile	Gly 245	Thr	Phe	Phe	Ile	Pro 250	Asp	Thr	Tyr	Asn	Pro 255	
Asp	Asp	Asp	Lys	Ile 260	Tyr	Phe	Phe	Phe	Arg 265	Glu	Ser	Ser	Gln	Glu 270	
Gly	Ser	Thr	Ser	Asp 275	Lys	Thr	Ile	Leu	Ser 280	Arg	Val	Gly	Arg	Val 285	
Cys	Lys	Asn	Asp	Val 290	Gly	Gly	Gln	Arg	Ser 295	Leu	Ile	Asn	Lys	Trp 300	
Thr	Thr	Phe	Leu	Lys 305	Ala	Arg	Leu	Ile	Cys 310	Ser	Ile	Pro	Gly	Ser 315	
Asp	Gly	Ala	Asp	Thr 320	Tyr	Phe	Asp	Glu	Leu 325	Gln	Asp	Ile	Tyr	Leu 330	
Leu	Pro	Thr	Arg	Asp 335	Glu	Arg	Asn	Pro	Val 340	Val	Tyr	Gly	Val	Phe 345	
Thr	Thr	Thr	Ser	Ser 350	Ile	Phe	Lys	Gly	Ser 355	Ala	Val	Cys	Val	Tyr 360	
Ser	Met	Ala	Asp	Ile 365	Arg	Ala	Val	Phe	Asn 370	Gly	Pro	Tyr	Ala	His 375	

[illegible]

[illegible]

				665					670					675
Ile	Val	Lys	Leu	Thr 680	Leu	Asn	Val	Ile	Glu 685	Asn	Glu	Gln	Met	Glu 690
Asn	Thr	Gln	Arg	Ala 695	Glu	His	Glu	Glu	Gly 700	Gln	Val	Lys	Asp	Leu 705
Leu	Ala	Glu	Ser	Arg 710	Leu	Arg	Tyr	Lys	Asp 715	Tyr	Ile	Gln	Ile	Leu 720
Ser	Ser	Pro	Asn	Phe 725	Ser	Leu	Asp	Gln	Tyr 730	Cys	Glu	Gln	Met	Trp 735
His	Arg	Glu	Lys	Arg 740	Arg	Gln	Arg	Asn	Lys 745	Gly	Gly	Pro	Lys	Trp 750
Lys	His	Met	Gln	Glu 755	Met	Lys	Lys	Lys	Arg 760	Asn	Arg	Arg	His	His 765
Arg	Asp	Leu	Asp	Glu 770	Leu	Pro	Arg	Ala	Val 775	Ala	Thr			

```
<210> 311
<211> 25
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.
```

```
<400> 311
caacgcagcc gtgataaaca agtgg 25
```

```
<210> 312
<211> 24
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.
```

```
<400> 312
gcttggacat gtaccaggcc qtqq 24
```

```
<210> 313
<211> 45
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.
```

<400> 313
ggccagactg atttgctcaa ttcctggaag tgatggggca gatac 45

<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

<400> 314
ccctgacctc cctgagccac actgagctgg aagccgcaga ggtcatcctg 50
gagcatgccc accgcgggga gcagacaacc tcccaggtaa gctggggagca 100
agacctgaag ctgtttcttc aggagcctgg tgtattttcc cccacccac 150
ctcagcagtt tcagccagca gggactgatc aggtgtgtgt cctggagtgg 200
ggagcagaag gcgtggctgg caagagtggc ctggagaaag aggttcagcg 250
cttgaccagc cgagctgccc gtgactacaa gatccagaac catgggcatc 300
gggtgaggtg ggggggcaca ggtgtcatgt gcaccttctt gtctcagcaa 350
gaagagctga gagaggggat cttggagcca ttgaggggtg catggagcta 400
cagaggggag ggaaaggat ttttaaggtaa cagtgtggca caatagttaa 450
gagcacagtt tttggagcta gaccgacata ggttcaaatt ctcttctgtt 500
gcttcttagt tctgtagccc caggtaaggg agtgacttaa cctctctgga 550
cttcaatttc ctcatcacta aagtagggcc aataatagca cccacctcat 600
aggggaagatt aaatgacata atgtatgtga tgcaactagc aaagtaccag 650
tcccatagta agtcatgccc cacagtattt ccaccaccc ctgttctctg 700
ccttcccaac caggtactgc aacgactgga gcagaggcgg cagcaggctt 750
cagagcggga ggctccaagc atagaacaga ggttacagga agtgcgagag 800
agcatccgcc gggcacaggt gagccaggtg aagggggctg cccggctggc 850
cctgctgcag ggggctggct tagatgtgga gcgctggctg aagccagcca 900
tgaccagggc ccaggatgag gtggagcagg agcggcggct cagtgaggct 950
cggctgtccc agagggacct ctctccaacc gctgaggatg ctgagctttc 1000
tgactttgag gaatgtgagg agacgggaga gctctttgag gagcctgccc 1050
ccaagccct ggccacgagg gccctcccct gccctgcaca cgtgggtattt 1100
cgctatcagg cagggcgtag gtagtgctg acaatcacgg agggtgagtg 1150
gctggaggtc atagaggagg gagatgctga cgaatgggtc aaggctcgga 1200
accagcacgg cgaggtaggc tttgtccctg agcgatatct caacttcccg 1250

gacctctccc tcccagagag cagccaagac agtgacaatc cctgcggggc 1300
 agagcccaca gcattcctgg cacaggccct gtacagctac accggacaga 1350
 gtgcagagga gctgagcttc cctgaggggg cactcatccg tctgctgccc 1400
 cgggcccacg atggagtaga tgacggcttc tggaggggag aatttggggg 1450
 ccgtgttggg gtcttcccct ccctgctggt ggaagagctg cttggccccc 1500
 cagggccacc tgaactctct gaccctgaac agatgctgcc gtcccttctt 1550
 cctcccagct tctcccacc tgcacctacc tctgtgttgg atgggcccc 1600
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<210> 315
<211> 370
<212> PRT
<213> Homo sapiens
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  1          5          10          15
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Val	Phe	Pro	Pro	Thr 20	Pro	Val	Leu	Cys	Leu 25	Pro	Asn	Gln	Val	Leu 30
Gln	Arg	Leu	Glu	Gln 35	Arg	Arg	Gln	Gln	Ala 40	Ser	Glu	Arg	Glu	Ala 45
Pro	Ser	Ile	Glu	Gln 50	Arg	Leu	Gln	Glu	Val 55	Arg	Glu	Ser	Ile	Arg 60
Arg	Ala	Gln	Val	Ser 65	Gln	Val	Lys	Gly	Ala 70	Ala	Arg	Leu	Ala	Leu 75
Leu	Gln	Gly	Ala	Gly 80	Leu	Asp	Val	Glu	Arg 85	Trp	Leu	Lys	Pro	Ala 90
Met	Thr	Gln	Ala	Gln 95	Asp	Glu	Val	Glu	Gln 100	Glu	Arg	Arg	Leu	Ser 105
Glu	Ala	Arg	Leu	Ser 110	Gln	Arg	Asp	Leu	Ser 115	Pro	Thr	Ala	Glu	Asp 120
Ala	Glu	Leu	Ser	Asp 125	Phe	Glu	Glu	Cys	Glu 130	Glu	Thr	Gly	Glu	Leu 135
Phe	Glu	Glu	Pro	Ala 140	Pro	Gln	Ala	Leu	Ala 145	Thr	Arg	Ala	Leu	Pro 150
Cys	Pro	Ala	His	Val 155	Val	Phe	Arg	Tyr	Gln 160	Ala	Gly	Arg	Glu	Asp 165
Glu	Leu	Thr	Ile	Thr 170	Glu	Gly	Glu	Trp	Leu 175	Glu	Val	Ile	Glu	Glu 180
Gly	Asp	Ala	Asp	Glu 185	Trp	Val	Lys	Ala	Arg 190	Asn	Gln	His	Gly	Glu 195
Val	Gly	Phe	Val	Pro 200	Glu	Arg	Tyr	Leu	Asn 205	Phe	Pro	Asp	Leu	Ser 210
Leu	Pro	Glu	Ser	Ser 215	Gln	Asp	Ser	Asp	Asn 220	Pro	Cys	Gly	Ala	Glu 225
Pro	Thr	Ala	Phe	Leu 230	Ala	Gln	Ala	Leu	Tyr 235	Ser	Tyr	Thr	Gly	Gln 240
Ser	Ala	Glu	Glu	Leu 245	Ser	Phe	Pro	Glu	Gly 250	Ala	Leu	Ile	Arg	Leu 255
Leu	Pro	Arg	Ala	Gln 260	Asp	Gly	Val	Asp	Asp 265	Gly	Phe	Trp	Arg	Gly 270
Glu	Phe	Gly	Gly	Arg 275	Val	Gly	Val	Phe	Pro 280	Ser	Leu	Leu	Val	Glu 285
Glu	Leu	Leu	Gly	Pro 290	Pro	Gly	Pro	Pro	Glu 295	Leu	Ser	Asp	Pro	Glu 300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala

305	310	315
Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly		
320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro		
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Pro Asp Pro Gly His Pro Asp Pro Leu Thr		
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<210> 316
 <211> 4407
 <212> DNA
 <213> Homo sapiens

<400> 316
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<210> 317
<211> 837
<212> PRT
<213> Homo sapiens

<400> 317
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35 40 45
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
50 55 60
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
65 70 75
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

Gly Val Leu Gln Tyr Arg Gly Ala Glu	Leu His Leu Gln Pro	Leu
155	160	165
Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His	Ile
170	175	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys	Asn
185	190	195
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg	Ala
200	205	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val	Val
215	220	225
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys	Arg
230	235	240
Tyr Leu Leu Thr Val Met Ala Ala Ala	Ala Lys Ala Phe Lys	His
245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu	Val
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser	Ala
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu	Asn
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile	Leu
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr	Leu
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser	Cys
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala	Ala
350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser	Lys
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His	Val
380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp	Ser
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly	Tyr
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu	Pro
425	430	435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln
440 445 450

Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro
455 460 465

Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
470 475 480

Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys
485 490 495

Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp
500 505 510

Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro
515 520 525

Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val
530 535 540

Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly
545 550 555

Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn
560 565 570

Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu
575 580 585

Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe
590 595 600

Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro
605 610 615

Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr
620 625 630

Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser
635 640 645

Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala
650 655 660

Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys
665 670 675

Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly
680 685 690

Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile
695 700 705

Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro
710 715 720

Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser

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Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp	740		745		750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr	755		760		765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro	770		775		780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg	785		790		795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro	800		805		810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu	815		820		825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys	830		835		

<210> 318
 <211> 23
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-23
 <223> Synthetic construct.

<400> 318
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<210> 319
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 319
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<210> 320
 <211> 43
 <212> DNA
 <213> Artificial

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 <223> Synthetic construct.

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<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

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<210> 322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

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Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	35	40	45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	50	55	60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	65	70	75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	80	85	90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	95	100	105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	110	115	120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	125	130	135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	140	145	150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	155	160	165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	170	175	180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	185	190	195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	200	205	210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	215	220	225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	230	235	240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	245	250	255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	260	265	270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
 275 280 285
 Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
 290 295 300
 Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
 305 310 315
 Arg Val

<210> 323
 <211> 1174
 <212> DNA
 <213> Homo sapiens

<400> 323
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 caggagctg cccggtcggc ctaggcaggc agccgcacca tggccagcac 100
 ggccgtgcag cttctgggct tctgtctcag cttcctgggc atggtgggca 150
 cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200
 accaacatcc tcacggccgt gtcctacctg aaagggtctt ggatggagtg 250
 tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300
 tggcgctgcc ccaagacctc caggctgcc gcgccctcat ggtcatctcc 350
 tgctgtctc cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400
 cacgcgctgc gccaaaggca caccgcgcaa gaccacctt gccatcctcg 450
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 gaggcaccct acaggcccta ccaggccccg cccagggccca ccacgaccac 700
 tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750
 gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800
 tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850
 gtccccggcg ggactgtcaa tggaggcagg ggttcagca caaagtttac 900
 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaatgt 950
 ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
230 235

<210> 325
<211> 2121
<212> DNA
<213> Homo sapiens

<400> 325
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cacatgccaa gtggtggcgt tctctctgtc catcctgggg ctggccggct 150
gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
aaccccgta cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250
gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcac 350
gtcctgggtg ccattggcct cctggtatcc atctttgccc tgaaatgcat 400
ccgcattggc agcatggagg actctgccaa agccaacatg aactgacct 450
ccgggatcat gtccattgtc tcaggtcttt gtgcaattgc tggagtgtct 500
gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550
gtacaccggc atgggtggga tgggtgcagac tgttcagacc aggtacacat 600
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gggggtgtga tgatgtgcat cgcctgccgg ggcctggcac cagaagaaac 700
caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
aagaagatat acgatggagg tgcccgaca gaggacgagg tacaatctta 850
tccttccaag cagactatg tgtaatgtc taagacctct cagcacgggc 900
ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950
atctcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
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gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200
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 ttctgctgtt tgaattttgt ctccccaccc ccaacttggc tagtaataaaa 1350
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 cccatgatct cggtttttctt aactgtgat cttaaaagtt accaaaccaa 1450
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500
 tcttattaca gcaacaccat tctaggagtt tctgagctc tccactggag 1550
 tcctctttct gtcgcggggc agaaattgtc cctagatgaa tgagaaaatt 1600
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
 taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggctgagg tgggaggatc acttgagccc agggagggtt gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
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 aggttaaaac taattcttta a 2121

<210> 326
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 326
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 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
 20 25 30
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80	85	90
Ala Ile Gly Leu Leu Val Ser Ile Phe	Ala Leu Lys Cys Ile Arg	
95	100	105
Ile Gly Ser Met Glu Asp Ser Ala Lys	Ala Asn Met Thr Leu Thr	
110	115	120
Ser Gly Ile Met Phe Ile Val Ser Gly	Leu Cys Ala Ile Ala Gly	
125	130	135
Val Ser Val Phe Ala Asn Met Leu Val	Thr Asn Phe Trp Met Ser	
140	145	150
Thr Ala Asn Met Tyr Thr Gly Met Gly	Gly Met Val Gln Thr Val	
155	160	165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala	Leu Phe Val Gly Trp Val	
170	175	180
Ala Gly Gly Leu Thr Leu Ile Gly Gly	Val Met Met Cys Ile Ala	
185	190	195
Cys Arg Gly Leu Ala Pro Glu Glu Thr	Asn Tyr Lys Ala Val Ser	
200	205	210
Tyr His Ala Ser Gly His Ser Val Ala	Tyr Lys Pro Gly Gly Phe	
215	220	225
Lys Ala Ser Thr Gly Phe Gly Ser Asn	Thr Lys Asn Lys Lys Ile	
230	235	240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp	Glu Val Gln Ser Tyr Pro	
245	250	255
Ser Lys His Asp Tyr Val		
260		

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
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 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tggtggaatg 150
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggcttt catgatggcc atccttggca 400
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgtttga ggagctctgt tctgctgctg 650
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atcgcacaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgctc 750
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850
 caaagaaact ttgattttact gttcttaact gcctaattctt aattacagga 900
 actgtgcata agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaaacct aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taaggtgggt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctcatataga gacatgctta 1150
 tatgggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgctttttcag ggaaatcatg gataggggtg aagaagggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400
 atcctcttct ccagagggt ttttttttct tgtgtattaa attaacattt 1450
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550
 gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgaggttt catcaatata aataaaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atTTTTgttc tGTGaaaaat aaatttccctt ctTgtaccat ttctgttttag 1850
 ttttactaaa atctgtaaat actgtatttt tctgttttatt ccaaatttga 1900
 tgaaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
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<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328
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 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
 200 205 210

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
215 220 225

<210> 329
<211> 1315
<212> DNA
<213> Homo sapiens

<400> 329
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gaccgctttc atcggcaaca gcatcgtggt ggcccagggt gtgtgggagg 150
gcctgtggat gtctgcgtg gtgcagagca ccggccagat gcagtgaag 200
gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
cgcttggtgc tcacctctgg gattgtcttt gtcattctcag gggctctgac 400
gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
acccctgggt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
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ctgcacttgc ccctcggggg ggtcccaggg cccagccat tacatggccc 600
gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650
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gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750
ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800
tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900
tctggatctt gacatgccca tcttagaagc cagtcaagct atggaactaa 950
tgcgagggt gcttgctgtg ctggctttgc aacaagacag actgtcccca 1000
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gctgcccccc atcctactca ggtctctgga gctcctctct tcacccctgg 1100
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cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccaggtcc 1200
cagctatgta gacccccgcc cccacctcca aactgcacc cttctgacct 1250

gccccctcg tctcaccccc ttacactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val					
				215					220					

<210> 331

<211> 1160

<212> DNA

[illegible]

<400> 331

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gtaaaggcaa	tggcatttta	tcccttgcaa	attgctgggc	tggttcttgg	150
gttccttggc	atgggtggga	ctcttgccac	aacccttctg	cctcagtggg	200
ggagtatcag	cttttgttgg	cagcaacatt	attgtctttg	agaggctctg	250
ggaagggtc	tggatgaatt	gcatccgaca	agccagggtc	cggttgcaat	300
gcaagttcta	tagctccttg	ttggctctcc	cgctgccc	ggaaacagcc	350
cgggccctca	tgtgtgtggc	tgttgctctc	tccttgatcg	ccctgcttat	400
tggcatctgt	ggcatgaagc	aggtccagtg	cacaggctct	aacgagaggg	450
ccaaagcata	ccttctggga	acttcaggag	tcctcttcat	cctgacgggt	500
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tttctacaac	ccagccatcc	acataggtca	gaaacgagag	ctgggagcag	600
cacttttct	tggctgggca	agcgtgctg	tcctcttcat	tggagggggg	650
ctgctttgtg	gattttgctg	ctgcaacaga	aagaagcaag	ggtacagata	700
tccagtgcct	ggctaccgtg	tgccacacac	agataagcga	agaaatacga	750
caatgcttag	taagacctcc	accagttatg	tctaatagcct	ccttttgggt	800
ccaagtatgg	actatggtca	atgtttttta	taaagtccctg	ctagaaactg	850
taagtatgtg	aggcaggaga	acttgcttta	tgtctagatt	tacattgata	900
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acattctgac	ttcaggtgta	ttaaatacat	tgactattgt	tggacccaat	1000
cgctgctcca	attttcatat	tctaaattca	agtataccca	taatcattag	1050
caagtgtaca	atgatggact	acttattact	ttttgacat	catgtattat	1100
ctgataagaa	tctaaagttg	aaattgatat	tctataacaa	taaaacatat	1150
acctattcta	1160				

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

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tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334
<211> 85
<212> PRT
<213> Homo sapiens

<400> 334
Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
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Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30
Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45
Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60
Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75
Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335
<211> 742
<212> DNA
<213> Homo sapiens

<400> 335
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ctgctcgcgc cccgcccga tggctgcctc ccccgcgcg cctgctgtcc 100
tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150
ggcataagtg gaaataaaact caagctgatg cttcaaaaac gagaagcacc 200
tggtccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250
tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300
cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350
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gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450
gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500
ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550
agcgattctc ttcatgtatc tcctaattgcc ttacactact tggtttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
 gaagagttaa aacaacacat gtaaagcct tttgatattt catgggaatg 700
 cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 336
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 Leu Ala Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
 20 25 30
 Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
 35 40 45
 Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
 50 55 60
 Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
 65 70 75
 Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
 80 85 90
 Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
 95 100 105
 Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
 110 115 120
 Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
 125 130 135
 Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
 140 145

<210> 337
 <211> 1310
 <212> DNA
 <213> Homo sapiens

<400> 337
 cggctcgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50
 agccgggcgc tcggtagcgc ggcgggcaag gcaggcgcca tgacctgat 100
 tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150
 ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
 gaccactgc ccagccgctc agggacccca acgcatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300
 cccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350
 ggggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400
 gctacggctg aaattcctca atgattcaga gcaggtggcc agggcctggc 450
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
 cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
 tgtccacgag agtcgggtccc ccaaattccc cctgcccgcc ggggtccgag 650
 cccggccctt ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
 tccccctgac cgccactctg ggccctggccg gcttcaccct gctcctcagt 800
 ctcttgccct ttgccatgta ccgcccgtag tgcctccgcg ggcgcttggc 850
 agcgtcgccg gcccttcggg accttgctcc ccgcgccgcg gcgggagctg 900
 ctgcctgccc agggccgcct ctccggcctg cctcttcccc ctgccctgga 950
 gccagccctt gcgccgcaga ggactcccgg gactggcgga ggccccgccc 1000
 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
 cgcactggga gtgggctcct cggggctcgg catctgctgt cgctgcctcg 1100
 gccccgggca gagccggggc gccccggggg cccgtcttag tgttctgccg 1150
 gaggaccag ccgcctccaa tccctgacag ctccctgggc tgagttgggg 1200
 acgccaggtc ggtgggaggc tggatgaagg gagcggggag gggcagagga 1250
 gttccccgga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaaaa 1300
 aaaaaaaaaa 1310

<210> 338
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 338
 Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
 1 5 10 15
 Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
 20 25 30
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
 35 40 45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp
				50					55					60
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg
				65					70					75
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr
				80					85					90
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu
				95					100					105
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp
				110					115					120
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly
				125					130					135
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly
				140					145					150
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys
				155					160					165
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro
				170					175					180
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile
				185					190					195
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu
				200					205					210
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala
				215					220					225
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala
				230					235					240
Phe	Ala	Met	Tyr	Arg	Pro									
				245										

<210> 339
 <211> 849
 <212> DNA
 <213> Homo sapiens

<400> 339
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 tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100
 caagacccta agaaccatca gccctcagct gcacctctc cctccaagg 150
 atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200
 tcaggccagc ctcacagtc gctgtgactt ggcccagtg ctgcagctgg 250

aggacttgga tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300
gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400
acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
gtccggagca cgggggatga acaactgggt agaatggagg ttgcactgtt 550
caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700
ccttccatt tacaactaaa actgaccaga gcccaggaa taaatggttt 750
tcttggttc ctccttactc ccatctggac ccagtcccct gggtcctgtc 800
tggtatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340
<211> 148
<212> PRT
<213> Homo sapiens

<400> 340
Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala
1 5 10 15
Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val
20 25 30
Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
35 40 45
Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
50 55 60
Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
65 70 75
Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
80 85 90
Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
95 100 105
Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
110 115 120
Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
125 130 135
Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

140

145

<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
ccctccaagg atgacaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

<400> 342
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 343
atctcaggcg gcatcctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
gtggatgcct gcaagaaggt tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

332

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 345
 agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346
 <211> 2575
 <212> DNA
 <213> Homo sapiens

<400> 346
 tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50
 actgagaacc caccagctca tcccagacac ctcatagcaa cctattttata 100
 caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
 aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtccct 200
 gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
 ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
 ttgcacacgc tgttgccaaa tgtcaggacc aggttaagtg actggcagaa 350
 aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400
 gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgccaa 450
 gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
 ctccagttcc tctgctgct cctgatgctg ggatgcgtcc tgatgatggg 550
 ggcgatgttg caccctcccc accacaccct gcaccagact gtcacagccc 600
 aagccagcaa gcacagccct gaagccaggt accgcctgga ctttggggaa 650
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 tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750
 tggccgtggc cttaccccag gccagaagga accagagcca gggcaggaga 800
 ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850
 cccaaagagg gactgggggg ctgatgagga cggggaggtg tctgaagaag 900
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 gtgtctgcag cagcaccctc aggacagcct gccacagcc agcgtcatcc 1050
 tctgtttcca tgatgaggcc tggtcactc tctgcggac tgtacacagc 1100

atcctcgaca cagtgccag ggccttcctg aaggagatca tcctcgtgga 1150
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cttcatggat gccactgcg agtgccaccc aggctggctg gagcccctcc 1350
tcagcagaat agctggtgac aggagccgag tggatatctcc ggtgatagat 1400
gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450
tggggtgttg gactggaagc tggatttcca ctgggaacct ttgccagagc 1500
atgtgaggaa ggccctccag tcccccataa gccccatcag gagccctgtg 1550
gtgcccggag aggtggtggc catggacaga cattacttcc aaaacactgg 1600
agcgtatgac tctcttatgt cgctgcgagg tggtgaaaac ctcgaactgt 1650
ctttcaaggc ctggctctgt ggtggctctg ttgaaatcct tcctgctct 1700
cgggtaggac acatctacca aaatcaggat tccattccc ccctcgacca 1750
ggaggccacc ctgaggaaca gggttcgcat tgctgagacc tggctggggt 1800
cattcaaaga aaccttctac aagcatagcc cagaggcctt ctccttgagc 1850
aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900
gggttgctcg acattccact ggtttctggc taatgtctac cctgagctgt 1950
acctatctga acccaggccc agtttctctg gaaagctcca caacactgga 2000
cttgggctct gtgcagactg ccaggcagaa ggggacatcc tgggctgtcc 2050
catggtgttg gtccttgca gtgacagccg gcagcaacag tacctgcagc 2100
acaccagcag gaaggagatt cactttggca gccacagca cctgtgcttt 2150
gctgtcaggc aggagcaggt gattcttcag aactgcacgg aggaaggcct 2200
ggccatccac cagcagcact gggacttcca ggagaatggg atgattgtcc 2250
acattctttc tgggaaatgc atggaagctg tggtgcaaga aaacaataaa 2300
gatttgtagc tgcgtccgtg tgatggaaa gcccgccagc agtggcgatt 2350
tgaccagata aatgctgtgg atgaacgatg aatgtcaatg tcagaaggaa 2400
aagagaatth tggccatcaa aatccagctc caagtgaacg taaagagctt 2450
atatatttca tgaagctgat ccttttgtgt gtgtgctcct tgtgttagga 2500
gagaaaaaag ctctatgaaa gaatatagga agtttctcct tttcacacct 2550

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly
260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His
275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile
290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile
305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg
320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro
335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg
350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr
365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly
380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly
395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln
410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg
425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu
440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala
455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu
470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu
485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His
500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp
515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg
530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe

	545		550		555
Gly Ser Pro Gln	His Leu Cys Phe Ala	Val Arg Gln Glu Gln	Val		
	560		565		570
Ile Leu Gln Asn	Cys Thr Glu Glu Gly	Leu Ala Ile His Gln	Gln		
	575		580		585
His Trp Asp Phe	Gln Glu Asn Gly Met	Ile Val His Ile Leu	Ser		
	590		595		600
Gly Lys Cys Met	Glu Ala Val Val Gln	Glu Asn Asn Lys Asp	Leu		
	605		610		615
Tyr Leu Arg Pro	Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg	Phe		
	620		625		630
Asp Gln Ile Asn	Ala Val Asp Glu Arg				
	635				

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 348
 ggagaggtgg tggccatgga cag 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 349
 ctgtcactgc aaggagccaa cacc 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 350
 tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351
 <211> 2524
 <212> DNA
 <213> Homo sapiens

<400> 351
 cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50
 ctcagacatg gaggccagga tgtggcctgc gctgctgctg tcccacctcc 100
 tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
 tcttcatcct cccctogaac cccaccagcc ccagcccgcc ccccgctgtg 200
 caggggaggg ccctcggccc cactcatgt gtgcgtgtgg gagcgagcac 250
 ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtccctg 300
 cctggcactg cccccccagc cccccatca ggctttgagg aggggccgcc 350
 ctcatcccaa taccctggg ctatcgtgtg gggcccacc gtgtctcgag 400
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 gtcacaatta ccatctccat catcattgtt ctctggcca ctggcatcat 650
 cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700
 agcaaggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750
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 accccaaggg ggctccagcc ttccagttga accggtgagg gcaggggcaa 900
 tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950
 tgggggtgcc ctctggatgg gtatgagga ggcaggcgtg gcctcccaca 1000
 gccctggcc ctccaaggg ggctggacca gctcctctct gggaggcacc 1050
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tccgggggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150
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 tcgcgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggccc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
 1 5 10 15
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
 20 25 30
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120
 Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
 ggccgttggt tggcgcgagg ctgaaggggtg tggcgcgagc agcgctggtg 50
 gttggccggc ggcgggccgg gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcaactgc cacagcaact 150
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200
tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccgggg 300
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
taccagggga agatgtactt ccccggttat ttccccaacg agctgcgaaa 400
catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
acctggcacc aggcagctgg ggaggaggcg agctctccag ggagggaccc 500
agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550
agtagcccc agaggcgctg ggagtgttgc caccgccctc ccctgaagtt 600
tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggcc 650
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750
acgtcgctg ctttggctat aactgcgagt agggctcagg catcacacc 800
acctgtcca gggccctact gtccctgggg tcccaggctc tccttgagg 850
gggctcccc ccttcacct ggctgtcatc gggtagggcg gggccgtggg 900
ttcaggggcg caccacttcc aagcctgtgt cccacaggtc ctcggcgcag 950
tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcacia 1000
gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050
cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgtc 1100
ctagaggggc tcccaggag gtggaacctc aaccagctc tgcgcaggag 1150
gcggtgcag tccttttctc cctcaaaggt ctccgacct cagctggagg 1200
cgggcatctt tcctaaaggg tcccatagg gtctggttcc acccatccc 1250
aggtctgtgg tcagagcctg ggagggttcc ctacgatgg taggggtgcc 1300
ccatggagg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350
tgaghtaagg ccgccctgac ctggaactca gggggagggg gtaaaggag 1400
agaggagggg ggctagggg tcctctagat cagtgggggc actgcaggtg 1450
gggctctccc tatacctggg acacctgctg gatgtcacct ctgcaaccac 1500
acccatgtgg tggtttcatg aacagaccac gctcctctgc cttctcctgg 1550

cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600
 ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650
 gcacaccctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700
 cataggacca cacgtcccag ctgggaggag aggcctgggg cccccaggga 1750
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 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900
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 cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggagggagg 2050
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100
 ctgcgggatg tgattaaagt cctgatgtt tctc 2134

<210> 356
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 356
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala
 1 5 10 15
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
 20 25 30
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
 35 40 45
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
 50 55 60
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
 65 70 75
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
 80 85 90
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
 95 100 105
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
 110 115 120
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln
 125 130 135
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatgtt 50
cctcttattt ctctcactgt gtgagctggc tgcagaagtt gctgcagaag 100
ttgagaaatc ctcatatggt cctgggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgtcc atactccata 250
gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
gaggtttctga cacactacaa catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
tcagattcat ctctcctga taatgaacaa ggcctcccca gagtatgaag 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctctttattc tgggtggacag tggatatgaa gaaaatggga aggtgatatc 650
atcttttcaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700
ctctagatga cgagtgggat acactgcca cagcagaagt ttccgtagag 750
catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800
aaatcgtaga tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
aactcaaate tcagagacac taaacaacag gatcactagg cctgccaacc 950
acacacacac gcacgtgcac acacgcacgc acgctgtcac acacacacgc 1000
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
tctcttcttc cttcttttaa atttcatatc ctcaactcct atccaatttc 1100
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
 200 205 210
 Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
 215 220 225
 Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
 230 235 240
 Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
 245 250 255
 Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
 260 265 270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
 ccagcagtgc ccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 362
 attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
 <211> 1777
 <212> DNA
 <213> Homo sapiens

<400> 363
 ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
 ccggcgcggg tggcgagag atcagaagcc tcttcccaa gccgagccaa 100
 cctcagcggg gacccgggct cagggacgcg gcggcggcgg cggcgactgc 150
 agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
 cccagacagc cggcgctggc tgtggctcgg gctggcggcg gcgcttgggc 250
 tcttgacagc tggagtatca gccttgggaag tatatacgcc aaaagaaatc 300
 ttctgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
 tagtacgact ggcggggtga cctcagtcct ctggagcttc cagccagagg 400
 gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
 cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
 tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550
 atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
 cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650
 tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700
 ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
 aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
 gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
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atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100
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cctgatatga ggagccagtg ttgcatgatg aaaagatggg atgattctac 1200
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caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300
tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350
ccttttaatc taagggttta agactgatta gtcttagcat ttactgtagt 1400
tggaggatgg agatgctatg atggaagcat acccaggggt gccttttagca 1450
cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccatttgg 1500
ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550
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tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
attagcaaag gataaatgcc gaaggctcact tcattctgga cacagttgga 1700
tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
<211> 269
<212> PRT
<213> Homo sapiens

<400> 364
Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
1 5 10 15
Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
20 25 30
Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
35 40 45
Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
50 55 60
Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
65 70 75
Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
80 85 90
Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
95 100 105

Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile
110 115 120

Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys
125 130 135

Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile
140 145 150

Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val
155 160 165

Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr
170 175 180

Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn
185 190 195

Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser
200 205 210

Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly
215 220 225

Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro^{*} Val Ile
230 235 240

Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile
245 250 255

Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn
260 265

<210> 365
<211> 1321
<212> DNA
<213> Homo sapiens

<400> 365
gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50
cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggg 100
ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcg ccccggcgca gtcccccgcg gcccccgacc ctgaggcgctc 250
gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccgc 300
agaccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtggggc caccgggcat 400
agtggttgga gtttctgtag atggaaaaga agtctgggtca gaaggtttag 450
gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650
 agattactga tttcccatTT aagtggaatt cgtcattatg aaaaggacat 700
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850
 ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaaat 950
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
 caggaagaaa acgagccagt gatttacaat agagcaaggt aatgaatac 1150
 cttctgctgt gtctagctat atcgcatctt aacactatTT tattaattaa 1200
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250
 gagcttttct acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 366
 Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
 1 5 10 15
 Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
 20 25 30
 Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
 35 40 45
 Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
 50 55 60
 Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
 65 70 75
 Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
 80 85 90

[illegible]

Trp	Ser	Pro	Gln	Thr 95	Pro	Ala	Pro	Pro	Cys 100	Ser	Arg	Cys	Phe	Ala 105
Arg	Ala	Ile	Glu	Ser 110	Ser	Arg	Asp	Leu	Leu 115	His	Arg	Ile	Lys	Asp 120
Glu	Val	Gly	Ala	Pro 125	Gly	Ile	Val	Val	Gly 130	Val	Ser	Val	Asp	Gly 135
Lys	Glu	Val	Trp	Ser 140	Glu	Gly	Leu	Gly	Tyr 145	Ala	Asp	Val	Glu	Asn 150
Arg	Val	Pro	Cys	Lys 155	Pro	Glu	Thr	Val	Met 160	Arg	Ile	Ala	Ser	Ile 165
Ser	Lys	Ser	Leu	Thr 170	Met	Val	Ala	Leu	Ala 175	Lys	Leu	Trp	Glu	Ala 180
Gly	Lys	Leu	Asp	Leu 185	Asp	Ile	Pro	Val	Gln 190	His	Tyr	Val	Pro	Glu 195
Phe	Pro	Glu	Lys	Glu 200	Tyr	Glu	Gly	Glu	Lys 205	Val	Ser	Val	Thr	Thr 210
Arg	Leu	Leu	Ile	Ser 215	His	Leu	Ser	Gly	Ile 220	Arg	His	Tyr	Glu	Lys 225
Asp	Ile	Lys	Lys	Val 230	Lys	Glu	Glu	Lys	Ala 235	Tyr	Lys	Ala	Leu	Lys 240
Met	Met	Lys	Glu	Asn 245	Val	Ala	Phe	Glu	Gln 250	Glu	Lys	Glu	Gly	Lys 255
Ser	Asn	Glu	Lys	Asn 260	Asp	Phe	Thr	Lys	Phe 265	Lys	Thr	Glu	Gln	Glu 270
Asn	Glu	Ala	Lys	Cys 275	Arg	Asn	Ser	Lys	Pro 280	Gly	Lys	Lys	Lys	Asn 285
Asp	Phe	Glu	Gln	Gly 290	Glu	Leu	Tyr	Leu	Arg 295	Glu	Lys	Phe	Glu	Asn 300
Ser	Ile	Glu	Ser	Leu 305	Arg	Leu	Phe	Lys	Asn 310	Asp	Pro	Leu	Phe	Phe 315
Lys	Pro	Gly	Ser	Gln 320	Phe	Leu	Tyr	Ser	Thr 325	Phe	Gly	Tyr	Thr	Leu 330
Leu	Ala	Ala	Ile	Val 335	Glu	Arg	Ala	Ser	Gly 340	Cys	Lys	Tyr	Leu	Asp 345
Tyr	Met	Gln	Lys	Ile 350	Phe	His	Asp	Leu	Asp 355	Met	Leu	Thr	Thr	Val 360
Gln	Glu	Glu	Asn	Glu 365	Pro	Val	Ile	Tyr	Asn 370	Arg	Ala	Arg		

<210> 367

<211> 30
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-30
 <223> Synthetic construct.

 <400> 367
 tggaaaagaa gtctgggtcag aagggttagg 30

 <210> 368
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 368
 catttggtt cattctcctg ctctg 25

 <210> 369
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

 <400> 369
 aaaacctcag aacaactcat ttgacacc 28

 <210> 370
 <211> 41
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-41
 <223> Synthetic construct.

 <400> 370
 gtctcaccat gggtgctctt gccaaattgt gggaagcagg g 41

 <210> 371
 <211> 1150
 <212> DNA
 <213> Homo sapiens

 <400> 371
 gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct	cgaggctggt	gggaagaagc	cgagatggcg	gcagccagcg	100
ctggggcaac	ccggctgctc	ctgctcttgc	tgatggcggt	agcagcgccc	150
agtcgagccc	ggggcagcgg	ctgccggggc	gggactggtg	cgcgaggggc	200
tggggcgga	ggtcgagagg	gcgaggcctg	tggcacggtg	gggctgctgc	250
tggagcactc	atttgagatc	gatgacagtg	ccaacttccg	gaagcggggc	300
tcactgctct	ggaaccagca	ggatggtacc	ttgtccctgt	cacagcggca	350
gctcagcgag	gaggagcggg	gccgactccg	ggatgtggca	gccctgaatg	400
gcctgtaccg	ggtccggatc	ccaaggcgac	ccggggccct	ggatggcctg	450
gaagctggtg	gctatgtctc	ctcctttgtc	cctgctgtgt	ccctggtgga	500
gtcgcacctg	tcggaccagc	tgaccctgca	cgtggatgtg	gccggcaacg	550
tgggtggcg	gtcggtggtg	acgcaccccg	ggggctgccg	gggccatgag	600
gtggaggacg	tggacctgga	gctgttcaac	acctcggtgc	agctgcagcc	650
gcccaccaca	gcccaggcc	ctgagacggc	ggccttcatt	gagcgcctgg	700
agatggaaca	ggcccagaag	gccaagaacc	cccaggagca	gaagtccttc	750
ttcgccaaat	actggatgta	catcattccc	gtcgtcctgt	tcctcatgat	800
gtcaggagcg	ccagacaccg	ggggccaggg	tgggggtggg	ggtgggggtg	850
gtggtggggg	tagtggcctt	tgctgtgtgc	cacctccct	gtaagtctat	900
ttaaaaacat	cgacgataca	ttgaaatgtg	tgaacgtttt	gaaaagctac	950
agcttccagc	agccaaaagc	aactgttgtt	ttggcaagac	ggtcctgatg	1000
tacaagcttg	attgaaattc	actgtctact	tgatacgtta	ttcagaaacc	1050
caaggaatgg	ctgtcccat	cctcatgtgg	ctgtgtggag	ctcagctgtg	1100
ttgtgtggca	gtttattaaa	ctgtcccca	gatcgacacg	caaaaaaaaa	1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu
1 5 10 15

Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
20 25 30

Arg Ala Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu
35 40 45

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
50 55 60
Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
65 70 75
Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
80 85 90
Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
95 100 105
Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
110 115 120
Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
125 130 135
Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
140 145 150
Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
155 160 165
Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
170 175 180
Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
185 190 195
Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
200 205 210
Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
215 220 225
Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
230 235 240
Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly
245 250 255
Gly Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu
260 265

<210> 373
<211> 1706
<212> DNA
<213> Homo sapiens

<400> 373
ggagcgcctgc tggaacccga gccggagccg gagccacagc ggggaggggtg 50
gcctggcgcc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100
cagcaggtcg tccggggggc caccatgctg gtgaactgcct accttgcttt 150
tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200

ctaaaccccc tgaaggggcc tgcagcaatc cctccttctc tcggttttcaa 250
ctggactttct atcaggtota cttcctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggctc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
cctctttctc ctgacttact cactatgctg ctttaaccaa ctctctcaag 500
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gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
tctggaacca tgtgctgggt gtagtggcag gtgtggcagc tgaggctgta 700
gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750
tctcctgggt ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
ctcctgtcgg accgccgctg gctgctgctg ggcaccatac aagctctatt 900
tgagagtgtc atcttcatct ttgtcttctc ctggacacct gtgctggacc 950
cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
ctgcttgggt cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150
tccttcatag cttttctact tattgagttg gcttgtggat tatactttct 1200
cagcatgagc ttctacgga gaaaggatgat ccctgagaca gagcaggctg 1250
gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagcatttgc tctgctgtca tggatgatggc tctgctggca gtgggtgggac 1400
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
gaggagccct atgccctga gctgtaacct cactccagga caagatagct 1500
gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
gggaggacat gatgggggtg atggactgga aagaaggctc caaaagttcc 1650

ctctgtgtta ctcccatTTta gaaaataaac actttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser	1	5	10	15
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly	20	25	30	
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	35	40	45	
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	50	55	60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	65	70	75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	80	85	90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	95	100	105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	110	115	120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala	125	130	135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala	140	145	150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu	155	160	165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val	170	175	180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp	185	190	195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu	200	205	210	
Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	215	220	225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	230	235	240	

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile
 245 250 255
 Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp
 260 265 270
 Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe
 275 280 285
 Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg
 290 295 300
 Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu
 305 310 315
 Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr
 320 325 330
 Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile
 335 340 345
 Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser
 350 355 360
 Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala
 365 370 375
 Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys
 380 385 390
 Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr
 395 400 405
 Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu
 410 415 420
 Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu
 425 430 435
 Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu
 440 445 450

<210> 375
 <211> 1098
 <212> DNA
 <213> Artificial

<400> 375
 gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50
 gccctggaga tgggtccccg cgccgcgggc tgggtgttgtc tcgtgctctg 100
 gctccccgcg tgcgtcgcgg cccacggctt ccgtatccat gattatttgt 150
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
 cctgccaagg actttggtgg tatctttcac acaaggtatg agcagattca 250

ccttggtcccc gctgaacctc cagaggcctg cggggaactc agcaacgggt 300
tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
ctctccaaga ctcggtggtt ccaggagcac ggcgggaggc cggatgatcat 400
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
acagtaccca gcgcacagct gacatccccg cctcttctct gctcggccga 500
gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
catcatttcc atcccagtcg atgtcaccag catccccacc tttgagctgc 600
tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
aatttgagga tagcatctgg ggacaagtgg agccaggtag agggaaaggg 750
tttgggcgtt gctaggctga aagggagcc acaccactgg ccttcccttc 800
cccaggcccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
ccccagggtt tctggctaga acccgaaaca aaaggagctg aaggcagggtg 900
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
taccagggtt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
aaagagctgg tggttgggga ctcaataaac cctcactgac tttttagcaa 1050
taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5					10					15
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20					25						30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35					40						45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
			50					55						60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
			65					70						75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
			80					85						90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
 95 100 105
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
 110 115 120
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
 125 130 135
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
 140 145 150
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
 155 160 165
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
 170 175 180
 Leu Gln Pro Pro Trp Thr Phe Trp
 185

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagaccacgg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val
 1 5 10 15
 Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
 20 25 30
 Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
 35 40 45
 Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
 50 55 60
 Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
 65 70 75
 Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
 80 85 90
 His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
 95 100 105
 Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
 110 115

<210> 379
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 379
 ctgcctccac tgctctgtgc tggg 24

<210> 380
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 380
 cagagcagtg gatgttcccc tggg 24

<210> 381
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt cttcttgat gggggcccag gggggccagg agagtataaa 50
 ggcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100
 gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
 ctctgggggg gcccacctg ggcaggggaag atgtatggcc ctggaggagg 200
 caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
 ggggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttga 300
 gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
 caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
 ctttctccg gggatggtc atgtacacca gcaaggaccg ctatttctat 450
 tttgggaagc ttgatggcca gatctcctct gcctaccca gccaaagagg 500
 gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcataaga 550
 gcattggcct tgaatggaat tatccactag aggagccgac cactgagcca 600
 ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650
 ggtatggggc catccgagct gaggccatct gtgtgggtgg ggctgatgg 700
 actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
 gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1				5					10					15
Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20					25					30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35					40					45

ttgaactctg gtgactatca agggaacgcg atgccccccc tccccctccc 2150
tctccctctc acttttggtg caagatcctt ccttgctcgt tttagtgcac 2200
tcataatact ggtcattttc ctctcatata taatcaaccc attgaaattt 2250
aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
<211> 513
<212> PRT
<213> Homo sapiens

<400> 385
Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
1 5 10 15
Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
20 25 30
Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
35 40 45
Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
50 55 60
Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
65 70 75
Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
80 85 90
Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
95 100 105
Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
110 115 120
Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
125 130 135
Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
140 145 150
Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
155 160 165
Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
170 175 180
Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
185 190 195
Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

200	205	210
His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe
215	220	225
Pro Arg Leu Val	Ser Leu Gln Asn Leu	Tyr Leu Gln Trp Asn Lys
230	235	240
Ile Ser Val Ile	Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu
245	250	255
Gln Arg Leu Asp	Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly
260	265	270
Pro Ser Val Phe	Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu
275	280	285
Asp Ser Asn Lys	Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser
290	295	300
Trp Ile Ser Leu	Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu
305	310	315
Cys Ser Arg Asn	Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe
320	325	330
Lys Gly Leu Arg	Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu
335	340	345
Leu Gln Gly Val	Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile
350	355	360
Cys Gly Lys Ser	Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu
365	370	375
Pro Lys Pro Thr	Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu
380	385	390
Ser Lys Pro Pro	Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly
395	400	405
Pro Glu Thr Asp	Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile
410	415	420
Ile Ala Gly Ser	Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu
425	430	435
Leu Val Ile Tyr	Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met Lys
440	445	450
Gln Leu Gln Gln	Arg Ser Leu Met Arg	Arg His Arg Lys Lys Lys
455	460	465
Arg Gln Ser Leu	Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe Tyr
470	475	480
Val Asp Tyr Lys	Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu Leu
485	490	495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
 500 505 510

Cys Glu Val

<210> 386
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 386
 ctgggatctg aacagtttcg gggc 24

<210> 387
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 387
 ggtccccagg acatggtctg tccc 24

<210> 388
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 388
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
 <211> 1449
 <212> DNA
 <213> Homo sapiens

<400> 389
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
 ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100
 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
 ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggtat atctggatcc tctgctgct ggttttggtg 250
gcagctcttc tctgtggagc tgtggctctc tgcctccagt gctggctgag 300
gagaccccca attgattctc acaggcgcac catggcagtt tttgctggtg 350
gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400
ggaattcacc ttcaaactca aaccctgac ctatatcctg ttctgctcc 450
atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500
caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
ggatgttgga aaaaattttg gtcattggaga tgtttaaata gtaaagtagc 700
aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
tctgctttaa actctttcct agcatggggc ccataaaaat tattataatt 900
taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100
tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
ccaacacggg gagaaaagaa aatttcccct ttacagtaa tgaatgtggc 1200
ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1				5					10					15

Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
20 25 30
Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
35 40 45
His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu
50 55 60
Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
65 70 75
Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
80 85 90
Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
95 100 105
Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
110 115 120
Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
125 130 135
Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
140 145

<210> 391
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 391
cttttcagtgcacctcagc gatctc 26

<210> 392
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 392
ccaaaacatg gagcaggaac agg 23

<210> 393
<211> 47
<212> DNA
<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 393
 ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 394
 gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
 acccaccggc gtttctccag ctgatcttg aggctgcttc gccagtgtgg 100
 gacgcagctg acgcccgtt attagctctc gctgcgtcgc ccgggtcag 150
 aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
 tctctttctac tttgggagag agagaaagtc agatgcccct tttaaactcc 250
 ctcttcaaaa ctcatctcct ggggtgactga gttaatagag tggatacaac 300
 cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
 ttttcaagtc ttgatttgtg gottacctca agttaccatt tttcagtcaa 400
 gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
 tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatttggg 500
 gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
 gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600
 tctagcagag gaaaataaga acacagtgga tgtcgagaac ggtgcttcta 650
 tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700
 attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
 gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800
 cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850
 ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900
 agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950
 aagctctaca cathttcaag gagtatgctg gattcatgga actctaattc 1000
 tgtacataaa aattttaaag ttatttgttt gctttcaggc aagtctgttc 1050
 aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150
aatgaaaac actgaaaaac atggattcat ttctataaca cttttattta 1200
agtatataac acgttttttg gacaagtga gaagtgttaa tcattctgtc 1250
atttgttctc aatagatgta actgttagac tacggctatt tgaaaaaatg 1300
tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350
tataatgttg aaaataatgt ttgaaatca tgacccaaag aatgtattga 1400
tttgactat ccttcagaat aactgaaggt taattattgt atatttttaa 1450
aaattacact tataagagta taatcttgaa atgggtagca gccactgtcc 1500
attacctatc gtaaacattg gggcaattta ataacagcat taaaatagtt 1550
gtaaactcta atcttatact tattgaagaa taaaagatat ttttatgatg 1600
agagtaacaa taaagtattc atgatttttc acatacatga atgttcattt 1650
aaaagtttaa tcttttgagt gtctatgcta tcaggaaagc acattatttc 1700
catatttggg ttaattttgc ttttattata ttggtctagg aggaaggac 1750
tttgagaat ggaactcttg aggactttag ccaggtgtat ataataaagg 1800
tacttttgtg ctgcattaaa ttgcttgga agtggttaaca ttatattata 1850
taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900
attcatttta tataatggcc acttaaaata agaacattta aaatataaac 1950
tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000
accctaactc tgggtaattc tagtataaaa caaattatac ttttatttaa 2050
atttccttg tagcaaatct aattgccaca tgggtgcccta tatttcatag 2100
tatttattct ctatagtaac tgcttaagtg cagctagctt ctagatttag 2150
actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200
catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250
tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300
acctttatgt gaagaaatta atttatgcc attgccaggt 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5					10					15

Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
 20 25 30
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
 35 40 45
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
 50 55 60
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
 65 70 75
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
 80 85 90
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
 95 100 105
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
 110 115 120
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
 125 130 135
 Ser Gly Ser Ile Arg
 140

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396
 cgcggccggg ccgcccgggt gagcgtgccg aggcggctgt ggcgcaggct 50
 tccagccccc accatgccgt gcccctgct gctgctgctg gccgtgagtg 100
 gggcccagac aaccggcca tgcttccccg ggtgccaatg cgaggtggag 150
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300
 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
 caccagcatc tcacccactg ccttctcccg ccttcgctac ctggagtcgc 400
 ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450
 agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500
 ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550
 acctctccca caacctcatt caccgctcg tgccccaccc cagaggggcc 600
 ggctgcctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

ccatgccgtg	cccaacctcc	gagacttgcc	cctgcgctac	ctgagcctgg	700
atgggaaccc	tctagctgtc	attggtccgg	gtgccttcgc	ggggctggga	750
ggccttacac	acctgtctct	ggccagcctg	cagaggctcc	ctgagctggc	800
gcccagtggc	ttccgtgagc	taccgggcct	gcaggctcctg	gacctgtcgg	850
gcaaccccaa	gcttaactgg	gcaggagctg	aggtgttttc	aggcctgagc	900
tccctgcagg	agctggacct	ttcgggcacc	aacctgggtgc	ccctgcctga	950
ggcgtgctc	ctccacctcc	cggcactgca	gagcgtcagc	gtggggccagg	1000
atgtgcggtg	ccggcgccctg	gtgcgggagg	gcacctaccc	ccggaggcct	1050
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tgccaggggc	cccaccatct	tgtgacaaat	ggtgtggccc	agggccacat	1150
aacagactgc	tgtcctgggc	tgctcaggt	cccgagtaac	ttatgttcaa	1200
tgtgccaaca	ccagtgggga	gcccgcaggc	ctatgtggca	gcgtcaccac	1250
aggagtgtg	ggcctaggag	aggctttgga	cctgggagcc	acacctagga	1300
gcaaagtctc	acccctttgt	ctacgttgct	tcccaaacc	atgagcagag	1350
ggacttcgat	gccaaaccag	actcgggtcc	cctcctgctt	cccttcccca	1400
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tgggctgagt	gtccccttgg	gcccattggc	cagtcaactca	ggggcgagtt	1550
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tcaagtccac	ccttctcatg	tgacagatgg	ggaaactgag	gccttgagaa	1700
ggaaaaaggc	taatctaagt	tcctgcgggc	agtggcatga	ctggagcaca	1750
gcctcctgcc	tcccagcccg	gacccaatgc	actttcttgt	ctcctctaata	1800
aagccccacc	ctccccgcct	gggctcccct	tgttgccctt	gcctgttccc	1850
cattagcaca	ggagtagcag	cagcaggaca	ggcaagagcc	tcacaagtgg	1900
gactctgggc	ctctgaccag	ctgtgcggca	tgggctaagt	cactctgccc	1950
ttcggagcct	ctggaagctt	agggcacatt	ggttcacagcc	tagccagttt	2000
ctcacccctg	gttggggctc	cccagcatcc	agactggaaa	cctaccatt	2050
ttcccctgag	catcctctag	atgtgcccc	aaggagttgc	tgcagttctg	2100

<210> 397
<211> 353
<212> PRT
<213> Homo sapiens

<400> 397
Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
1 5 10 15
Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
20 25 30
Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
35 40 45
Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
50 55 60
Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
65 70 75
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
80 85 90
Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
95 100 105
Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
110 115 120
Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
125 130 135
Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
140 145 150

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser
155 160 165

His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly
170 175 180

Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg
185 190 195

Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu
200 205 210

Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe
215 220 225

Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
230 235 240

Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly
245 250 255

Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala
260 265 270

Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp
275 280 285

Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
290 295 300

His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg
305 310 315

Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly
320 325 330

Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser
335 340 345

Ala Ala Arg Gly Pro Thr Ile Leu
350

<210> 398
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 398
ccctgccagc cgagagcttc acc 23

<210> 399
<211> 23
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgcag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtagct acgttggtt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600

tgctgcctcc tgcgccattt gctaagactc tatctggaca gggatatttaa 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgcccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
acctgcagag gaggcagac cccaaaccac catctcttta ctgtactagt 1000
cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050
tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag 1100
atTTTTgtaa tatctttctg ctattggata tatttattag ttaatatatt 1150
tatttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
ctttaaaaaa attcacagat tataattata acctgactag agcaggtgat 1250
gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
ccaaaaaaaa aaaaaaaaaa a 1571

<210> 402
<211> 261
<212> PRT
<213> Homo sapiens

<400> 402
Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
1 5 10 15
Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
20 25 30
Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
35 40 45
Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
50 55 60
Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
65 70 75
Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
80 85 90

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
95 100 105
Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
110 115 120
Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
125 130 135
Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
140 145 150
Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
155 160 165
Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
170 175 180
Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser
185 190 195
Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu
200 205 210
Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys
215 220 225
Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln
230 235 240
Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln
245 250 255
Trp Met Glu Glu Thr Glu
260

<210> 403
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 403
ctcctgtggt ctccagattt caggccta 28

<210> 404
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcgat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tccccttttg aaatcagtca ttggagggat gatggctggg gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaattggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650
accacttatg atacagtga aactacttg gtattgaata caccattga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aagggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggtg agaattgaccc cttggtcaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttta 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

[illegible]

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
cgcggtatccc gttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
gcggaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcgc gcgcctgaag tcggcggtggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150
tagataattt tcgttgccca gaatgtgaat gtattgactg gaggtagaga 200
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350
ataaatgctg tatccaatgc tcaggtaga ggtgatagct atgaaagcgg 400
ctgttttagga agaacaggtg ctcgagtttg gcttttcatt ggtttcatgt 450
tgatgttttg gtcacttatt gcttccatgt ggattctttt tggtagatat 500
gttaccctaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

380

tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600
agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650
tctgtttgta gatagggttt ttatctctca gtacacattg ccaaattggag 700
tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750
ttgaaatagt tttatgaaat ttctttattt ttcattgcat agactgttaa 800
tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850
tattcctgag atttagaact tgatctactc cctgagccag gggttacatca 900
tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacgggtg 950
gctcatgcct gtaatccag cactttggga ggccgaggcg ggccgattgc 1000
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cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
aggttgagct gagctgagtt tgcgccactg cactctagcc tgggggagaa 1200
agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
cataaaagggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
ttttttggta aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
tttatataat gattttttta atgccc aaag gactagtttg aaagcttctt 1450
ttaaaaaagaa ttcctcta atgacttttat gtgagaa 1487

<210> 410
<211> 158
<212> PRT
<213> Homo sapiens

<400> 410
Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
1 5 10 15
Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
20 25 30
Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
35 40 45
Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
50 55 60
Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
155

<210> 411
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 411
gtttgaggaa gctgggatac 20

<210> 412
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 412
ccaaactcga gcacctgttc 20

<210> 413
<211> 40
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 413
atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
 <223> Synthetic construct.

 <400> 416
 gccatagtca cgacatggat g 21

 <210> 417
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 417
 ggatggccag agctgctg 18

 <210> 418
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 418
 aaagtacaag tgtggcctca tcaagc 26

 <210> 419
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 419
 tctgactcct aagtcaggca ggag 24

 <210> 420
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 420
 attctctcca cagacagctg gttc 24

<210> 421
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

<400> 421
 gtacaagtgt ggcctcatca agccctgccc agccaactac ttgcg 46

<210> 422
 <211> 1701
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 1528
 <223> unknown base

<400> 422
 gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
 tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
 tggagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
 cagccagga gctcgtctgc tctctctctc tctctctcac tctcctctcc 200
 ctctctctct gctctgctta gtcctctagt cctcaaattc ccagtcccct 250
 gcacccttct ctgggacact atgttggttct ccgccctcct gctggagggtg 300
 atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
 acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
 cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
 ttgcctgtct tgcagcccca cggatatgac cagcctggca ccgagccttt 500
 ggacctgcac aacaatggcc acacagtgc actctctctg ccctctacct 550
 tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
 cactggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
 tgaagccaca ttgagagagc tccacattgt acattatgac tctgattcct 700
 atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
 ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
 tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa	cctaagagag	ctgctcccca	aacagctggg	gcagtacttc	900
cgctacaatg	gctcgctcac	aactccccct	tgctaccaga	gtgtgctctg	950
gacagttttt	tatagaaggt	cccagatttc	aatggaacag	ctggaaaagc	1000
ttcaggggac	attgttctcc	acagaagagg	agccctctaa	gcttctggta	1050
cagaactacc	gagcccttca	gcctctcaat	cagcgcatgg	tctttgcttc	1100
tttcatccaa	gcaggatcct	cgtataccac	aggtgaaatg	ctgagtctag	1150
gtgtaggaat	cttggttggc	tgtctctgcc	ttctcctggc	tgttttatttc	1200
attgctagaa	agattcggaa	gaagaggctg	gaaaaccgaa	agagtgtggg	1250
cttcacctca	gcacaagcca	cgactgaggc	ataaattcct	tctcagatac	1300
catggatgtg	gatgacttcc	cttcatgcct	atcaggaagc	ctctaaaatg	1350
gggtgtagga	tctggccaga	aacactgtag	gagtagtaag	cagatgtcct	1400
ccttcccctg	gacatctctt	agagaggaat	ggaccaggc	tgtcattcca	1450
ggaagaactg	cagagccttc	agcctctcca	aacatgtagg	aggaaatgag	1500
gaaatcgctg	tgttgttaat	gcagaganca	aactctgttt	agttgcaggg	1550
gaagtttggg	atatacccca	aagtcctcta	ccccctcact	tttatggccc	1600
tttccctaga	tatactgcgg	gatctctcct	taggataaag	agttgctggt	1650
gaagttgtat	atTTTTgatc	aatatatttg	gaaattaaag	tttctgactt	1700
t 1701					

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<210> 423
<211> 337
<212> PRT
<213> Homo sapiens
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<400> 423
Met  Leu  Phe  Ser  Ala  Leu  Leu  Leu  Glu  Val  Ile  Trp  Ile  Leu  Ala
  1      5      10
Ala  Asp  Gly  Gly  Gln  His  Trp  Thr  Tyr  Glu  Gly  Pro  His  Gly  Gln
      20      25      30
Asp  His  Trp  Pro  Ala  Ser  Tyr  Pro  Glu  Cys  Gly  Asn  Asn  Ala  Gln
      35      40      45
Ser  Pro  Ile  Asp  Ile  Gln  Thr  Asp  Ser  Val  Thr  Phe  Asp  Pro  Asp
      50      55      60
Leu  Pro  Ala  Leu  Gln  Pro  His  Gly  Tyr  Asp  Gln  Pro  Gly  Thr  Glu
      65      70      75
Pro  Leu  Asp  Leu  His  Asn  Asn  Gly  His  Thr  Val  Gln  Leu  Ser  Leu

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80					85					90				
Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala
				95					100					105
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly
				110					115					120
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His
				125					130					135
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala
				140					145					150
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu
				155					160					165
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His
				170					175					180
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro
				185					190					195
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe
				200					205					210
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val
				215					220					225
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln
				230					235					240
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro
				245					250					255
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn
				260					265					270
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr
				275					280					285
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly
				290					295					300
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile
				305					310					315
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser
				320					325					330
Ala	Gln	Ala	Thr	Thr	Glu	Ala								
				335										

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial


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<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
    gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
    cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
    ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
    cagaaaccca tgatacccta ctgaacaccg aatccccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
    aattttttcac cagagtaaacc ttgagaaacc aactggacct tgagtattgt 50
    acatttttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
    gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

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aacctgcttt gggactccct cccacaaaac tggtccgga tcaggaaca 200
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300
 ctgctgcagg aatgacacct ggtaccaga cccaccatt gaccctggga 350
 gggttgaatg tacaacagca actgcacca catgtgttac caatttttgt 400
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcattctg 500
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
 agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc 600
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaata 700
 agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagtgcct 750
 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
 tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 429
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
 1 5 10 15
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
 20 25 30
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
 35 40 45
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
 50 55 60
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
 65 70 75

Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn
80 85 90

Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr
95 100 105

Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro
110 115 120

Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly
125 130 135

Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp
140 145 150

Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln
155 160 165

Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp
170 175 180

Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His
185 190 195

Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln
200 205

<210> 430
<211> 1257
<212> DNA
<213> Homo Sapien

<400> 430
ggagagaggc gcgcgggtga aaggcgcatt gatgcagcct gcggcggcct 50
cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
ctgcagctgc ccgcgccgtc gagcgccctc gagatcccca aggggaagca 250
aaaggcgag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450
actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550
agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgcaactt cttctgtgga aggactttgt gaaggaattg 750
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcattcattat 850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900
ttattatgcc ttggaatggt tcacttaaata gacattttta ataagtttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
aatttgtaaa tgtaagaat tttttttata tctgttaaata aaaaattatt 1250
tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
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Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150
Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165
Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180
Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195
Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210
Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225
Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

<210> 432
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 432
aggacttgcc ctcaggaa 18

<210> 433
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 433
cgcaggacag ttgtgaaaat a 21

<210> 434
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 434
atgacgctcg tccaaggcca c 21

<210> 435

<211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 435
 cccacctgta ccaccatgt 19

 <210> 436
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 436
 actccaggca ccatctgttc tccc 24

 <210> 437
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 437
 aagggtggc attcaagtc 19

 <210> 438
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 438
 tgacctggca aaggaagaa 19

 <210> 439
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 439
 cagccaccct ccagtccaag g 21

 <210> 440
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 440
gggtcgtgtt ttggagaga 19

<210> 441
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 441
ctggccctca gagcaccaat 20

<210> 442
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 442
tcctccatca cttcccctag ctcca 25

<210> 443
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
ctggcaggag ttaaagttcc aaga 24

<210> 444
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
aaaggacacc gggatgtg 18

<210> 445
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<400> 445
  agcgtacact ctctccaggc aaccag 26

<210> 446
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 446
  caattctgga tgaggtggta ga 22

<210> 447
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 447
  caggactgag cgcttgttta 20

<210> 448
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 448
  caaagcgcca agtaccggac c 21

<210> 449
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 449
  ccagacctca gccaggaa 18

<210> 450
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 450
  ccctagctga ccccttca 18

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<210> 451
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 451
 tctgacaagc agttttctga atc 23

<210> 452
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 452
 ctctccccct cccttttctt ttgttt 26

<210> 453
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 453
 ctctggtgcc cacagtga 18

<210> 454
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 454
 ccatgcctgc tcagccaaga a 21

<210> 455
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 455
 caggaaatct ggaaacctac agt 23

<210> 456
 <211> 20
 <212> DNA

<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 456
ccttgaaaag gacccagttt 20
<210> 457
<211> 22
<212> DNA
<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
<400> 457
atgagtcgca cctgctgttc cc 22
<210> 458
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 458
tagcagctgc ccttggtta 18
<210> 459
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 459
aacagcaggt gcgactcatc ta 22
<210> 460
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic oligonucleotide probe
<400> 460
tgctaggcga cgacacccag acc 23
<210> 461
<211> 18
<212> DNA
<213> Artificial Sequence
<220>

<223> Synthetic oligonucleotide probe

<400> 461
tggacacgtg gcagtgga 18

<210> 462
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 462
tcatggtctc gtcccatc 19

<210> 463
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 463
caccatttgt ttctctgtct ccccatc 27

<210> 464
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 464
ccggcatcct tggagtag 18

<210> 465
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 465
tccccattag cacaggagta 20

<210> 466
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 466

aggctcttgc ctgtcctgct gct 23

- <210> 467
- <211> 18
- <212> DNA
- <213> Artificial Sequence

- <220>
- <223> Synthetic oligonucleotide probe

<400> 467
gccagagtc ccacttgt 18

- <210> 468
- <211> 19
- <212> DNA
- <213> Artificial Sequence

- <220>
- <223> Synthetic oligonucleotide probe

<400> 468
actgctccgc ctactacga 19

- <210> 469
- <211> 20
- <212> DNA
- <213> Artificial Sequence

- <220>
- <223> Synthetic oligonucleotide probe

<400> 469
aggcatcctc gccgtcctca 20

- <210> 470
- <211> 19
- <212> DNA
- <213> Artificial Sequence

- <220>
- <223> Synthetic oligonucleotide probe

<400> 470
aaggccaagg tgagtccat 19

- <210> 471
- <211> 20
- <212> DNA
- <213> Artificial Sequence

- <220>
- <223> Synthetic oligonucleotide probe

<400> 471
cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 472
tcaggggtcta catcagcctc ctgc 24

<210> 473
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 473
aaggccaagg tgagtccat 19

<210> 474
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 474
cctactgagg agccctatgc 20

<210> 475
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 475
tccaggtgga cccacttca gg 22

<210> 476
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 476
gggaggctta taggcccaat ctgg 24

<210> 477
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50